# STIC Search Report
## Biotech-Chem Library

## STIC Database Tracking Number: 142287

**TO: Elizabeth McElwain**
**Location: REM/2A11/2C18**
**Art Unit: 1638**
**Tuesday, January 25, 2005**

**Case Serial Number: 10/070666**

**From: Mary Jane Ruhl**
**Location: Biotech-Chem Library**
**Remsen 1-A-62**
**Phone: 571-272-2524**

**maryjane.ruhl@uspto.gov**

## Search Notes

Examiner McElwain,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

**STIC-Biotech/ChemLib** 142287

**From:** McElwain, Elizabeth
**Sent:** Tuesday, January 11, 2005 4:06 PM
**To:** STIC-Biotech/ChemLib
**Subject:** sequence search

Please search 10/070,666 - SEQ ID NO: 1 for prior art only

Thank you,
Beth

Elizabeth F. McElwain, Ph.D.
U.S. Patent and Trademark Office
Tech Center 1600, Art Unit 1638
room Remsen 2A11
mailbox Remsen 2C18
571-272-0802
elizabeth.mcelwain@uspto.gov



**********
STAFF USE ONLY

Searcher:_____
Searcher Phone: 2-
Date Searcher Picked up:____
Date Completed:_____
Searcher Prep/Rev. Time:___
Online Time:_____

**********
Type of Search
NA Sequence: #_____
AA Sequence :#_____
Structure: #_____
Bibliographic:_____
Litigation:_____
Patent Family:_____
Other:_____

**********
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other(Specify):_____

GenCore version 5.1.6


OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 06:21:29 ; Search time 4402 Seconds
(without alignments)
10090.875 Million cell updates/sec

Title: US-10-070-666A-1
Perfect score: 1219
Sequence: 1 agtaagcaaactaaatttaa.....taacaaaaaaaaaaaaaaaa 1219

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| | 1 | 615.4 | 50.5 | 659 | 4 | BM399473 | BM399473 5009-0-58 |
| | 2 | 68.2 | 5.6 | 1101 | 9 | CNS00EVL | AL069706 Drosophil |
| | 3 | 66.8 | 5.5 | 1101 | 9 | CNS0039G | AL063921 Drosophil |
| c | 4 | 65.8 | 5.4 | 1101 | 9 | CNS0039G | AL063921 Drosophil |
| c | 5 | 62 | 5.1 | 928 | 9 | CNS00DKY | AL071865 Drosophil |
| c | 6 | 61.8 | 5.1 | 1101 | 9 | CNS00EPO | AL069493 Drosophil |
| c | 7 | 61.4 | 5.0 | 1201 | 9 | CNS0167M | AL106396 Drosophil |
| | 8 | 60.4 | 5.0 | 886 | 8 | BH177277 | BH177277 008_L_22- |
| | 9 | 60.4 | 5.0 | 886 | 9 | CNS07JUX | AL614235 T3 end of |
| | 10 | 60.4 | 5.0 | 961 | 9 | CNS008HI | AL051882 Drosophil |
| c | 11 | 60.2 | 4.9 | 1101 | 9 | CNS00EVL | AL069706 Drosophil |
| c | 12 | 60 | 4.9 | 1101 | 9 | CNS001FB | AL060732 Drosophil |
| | 13 | 59.8 | 4.9 | 945 | 9 | CNS04D0K | AL285149 Tetraodon |
| c | 14 | 59.2 | 4.9 | 1101 | 9 | CNS00KAE | AL077628 Drosophil |
| | 15 | 58.8 | 4.8 | 1324 | 9 | AG376784 | AG376784 Mus muscu |
| | 16 | 58.4 | 4.8 | 1101 | 9 | CNS00Z2U | AL097152 Drosophil |
| | 17 | 58 | 4.8 | 1101 | 9 | CNS00BO1 | AL057419 Drosophil |
| | 18 | 57.6 | 4.7 | 1013 | 9 | CNS06RPQ | AL412260 T7 end of |
| c | 19 | 57.6 | 4.7 | 1101 | 9 | CNS00EO7 | AL069440 Drosophil |
| c | 20 | 56.6 | 4.6 | 945 | 9 | CNS04D0K | AL285149 Tetraodon |
| | 21 | 56 | 4.6 | 1201 | 9 | CNS0167M | AL106396 Drosophil |
| c | 22 | 55.6 | 4.6 | 1013 | 9 | CNS06RPQ | AL412260 T7 end of |
| c | 23 | 55.6 | 4.6 | 1101 | 9 | CNS0021J | AL061936 Drosophil |
| c | 24 | 55.4 | 4.5 | 1101 | 9 | CNS00BEU | AL056987 Drosophil |
| | 25 | 55.2 | 4.5 | 1043 | 9 | CNS0145P | AL103735 Drosophil |
| | 26 | 55.2 | 4.5 | 1101 | 9 | CNS00FVE | AL071298 Drosophil |
| | 27 | 55.2 | 4.5 | 1101 | 9 | CNS00KAE | AL077628 Drosophil |
| | 28 | 55.2 | 4.5 | 1206 | 5 | BQ709824 | BQ709824 AGENCOURT |
| c | 29 | 55 | 4.5 | 1101 | 9 | CNS003BD | AL064091 Drosophil |
| | 30 | 54 | 4.4 | 928 | 9 | CNS00DKY | AL071865 Drosophil |
| | 31 | 53.8 | 4.4 | 839 | 8 | AQ892711 | AQ892711 HS_4832_A |
| c | 32 | 53.8 | 4.4 | 900 | 8 | BH135675 | BH135675 ENTNT31TF |
| c | 33 | 53.8 | 4.4 | 1101 | 9 | CNS002B4 | AL062483 Drosophil |
| | 34 | 53.6 | 4.4 | 1101 | 9 | CNS0039L | AL063926 Drosophil |
| c | 35 | 53.6 | 4.4 | 1101 | 9 | CNS008WC | AL052719 Drosophil |
| | 36 | 53.6 | 4.4 | 1210 | 9 | CG749728 | CG749728 P044-1-C0 |
| c | 37 | 53.4 | 4.4 | 914 | 9 | CNS00ZJY | AL097768 Drosophil |
| | 38 | 53.4 | 4.4 | 1101 | 9 | CNS00FMC | AL070972 Drosophil |
| c | 39 | 53.4 | 4.4 | 1146 | 9 | CNS021G2 | AL176843 Tetraodon |
| | 40 | 53.2 | 4.4 | 1101 | 9 | CNS0177R | AL107697 Drosophil |
| | 41 | 53 | 4.3 | 1101 | 9 | CNS00LVZ | AL078819 Drosophil |
| c | 42 | 53 | 4.3 | 1168 | 9 | CL078758 | CL078758 CH216-153 |
| | 43 | 52.8 | 4.3 | 477 | 6 | CD135036 | CD135036 MG1-0036U |
| c | 44 | 52.8 | 4.3 | 1101 | 9 | CNS00EJ4 | AL069257 Drosophil |
| c | 45 | 52.8 | 4.3 | 1101 | 9 | CNS00EQL | AL069526 Drosophil |

ALIGNMENTS

RESULT 1
BM399473
LOCUS BM399473 659 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-58-B08.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM399473
VERSION BM399473.1 GI:18199526
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 659)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .659
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN

Query Match 50.5%; Score 615.4; DB 4; Length 659;
Best Local Similarity 99.8%; Pred. No. 1e-112;
Matches 616; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 AGTAAGCAAACTAAATTTAAAAAACAAGCATTATGGGAGTTGATAAGACTTAAGAAGAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         43 AGTAAGCAAACTAAATTTAAAAAACAAGCATTATGGGAGTTGATAAGACTTAAGAAGAAA 102

Qy         61 TTGTTCTTGAAAATAAACCCGAACTTCTCAACGAATACAAATTTATTTACAAGGATACTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        103 TTGTTCTTGAAAATAAACCCGAACTTCTCAACGAATACAAATTTATTTACAAGGATACTG 162

Qy        121 AATATGACTGCACTGAATATGCTAAATCAAATAAGCATCCTGGCGGTCTTAATTTCCTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 AATATGACTGCACTGAATATGCTAAATCAAATAAGCATCCTGGCGGTCTTAATTTCCTCA 222

Qy        181 ATTTGTTTATTGATGAGAAGTAAGATTTGACTGAATATTTCAGAACACTCCATTCTAAGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        223 ATTTGTTTATTGATGAGAAGTAAGATTTGACTGAATATTTCAGAACACTCCATTCTAAGT 282

Qy        241 AGGCTTTGAAAATTTTAAAATCCTTCCCTAAGACTGGCGCAAAATAAGAGGAGACTGAAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 AGGCTTTGAAAATTTTAAAATCCTTCCCTAAGACTGGCGCAAAATAAGAGGAGACTGAAT 342

Qy        301 CTTCAAAGAGATTCTCAATATTAAAGAAAAAGCTTAAGCATTTATTCGAACCAAACTGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 CTTCAAAGAGATTCTCAATATTAAAGAAAAAGCTTAAGCATTTATTCGAACCAAACTGGC 402

Qy        361 CTATCGAAATTGGTTTATTCTTAACTACCTTTACTTTATTTGTCACTGGATGTTTGACTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 CTATCGAAATTGGTTTATTCTTAACTACCTTTACTTTATTTGTCACTGGATGTTTGACTC 462

Qy        421 AAAAGTGGTATTTCTCTATTCCCCTTCTTGTCTTAATGCAAATCATCAGTGGTTGGATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 AAAAGTGGTATTTCTCTATTCCCCTTCTTGTCTTAATGCAAATCATCAGTGGTTGGATTG 522

Qy        481 GTCACTCTATGAACCACAATCGTAACCCTATATTAAGAAAATTCGCTTTAGTCTACGCTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 GTCACTCTATGAACCACAATCGTAACCCTATATTAAGAAAATTCGCTTTAGTCTACGCTC 582

Qy        541 CTCTTTGTGGTGGTTTCTCTAATAAATGGTGGGGTAGGAAGCACAATCAACATCATATGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 CTCTTTGTGGTGGTTTCTCTAATAAATGGTGGGGTAGGAAGCACAATCAACATCATATGT 642

Qy        601 TCACAAACAACATTCTA 617
              |||||||||||||||||
Db        643 CCACAAACAACATTCTA 659


RESULT 2
CNS00EVL
LOCUS       CNS00EVL                1101 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC:
            BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL069706
VERSION     AL069706.1  GI:4949849
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES            Location/Qualifiers
     source         1. .1101
                    /organism="Drosophila melanogaster"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:7227"
                    /clone="BACR29B23"
                    /clone_lib="RPCI-98"
                    /note="end : T7"
ORIGIN

  Query Match             5.6%;  Score 68.2;  DB 9;  Length 1101;
  Best Local Similarity   31.5%;  Pred. No. 0.0022;
  Matches  192;  Conservative  115;  Mismatches  299;  Indels    3;  Gaps    1;

Qy        610 ACATTCTAAAGGACGAAGATATCTAACACGATTACAAATTGTGGTAATTCCCCTTCTTAT 669
              |: :|: ::: : : ::| :|| : ||:| :| :::: |: :::|
Db        459 AHTWTMMMMMMWWAATWTWWAAAWAAAWTTATWAATWAAAAAWAWWWWATTTTTWWWWWT 518

Qy        670 TTTTAAAGTGGAAATTAGACTCCATCTTAGCTTCTTATTATGAATTTGAAGGAATCTTCC 729
              : ||:  :  : :| : |    |  :|  | | | ::  |: | ||  | |  :
Db        519 WATTWTTTWAWWTWTAWTAAAAAAAAAWATAATTTAAAWWAATAWATTAAWAATTTAWAA 578

Qy        730 TTGCCTTGCACTGGGTATTATTATTCAACTAAAACTTCTATATCGTAATTCTTTCTGAAT 789
              ::   |  | :   | |:|:||| |  ||||      | |  :|     || | |||
Db        579 WWTATATTAATWTATAAATWTWATTAATATAAAAAAATATTTTTTWATAAAATTTTTAAT 638

Qy        790 TGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTGGAAATCATGAAAATGAAATGAAAT 849
              ||  |  :|| || | |  :|   |: :|  |  ||    | :|||| :||  |||
Db        639 AATTTAATTAWTTATTAAATAAWTWATTWWWTAATTAAATAATTTWAAATAWAAAAAAAA 698

Qy        850 TCGAAAGAAGAATCACTTTACCATTTTTCGAACATCAAATAGCTGCAAGCAGAAACTACG 909
              ||| :| :|  | |:    ||  :|  ||    :||||     |:    |:: ||
Db        699 AAAAAAAWATWAAWAATWATAWATAAWTTAAAA---WAATAAAAWAAWAATWAWWATAAT 755

Qy        910 CTTTCCACGACATATTCTCTCTACTTATTATGGGTGGTATGTAATATTAGACTGAACATC 969
              |::  |    :| :| : : |:  :::|||    |   || :||:|: :      | ||
Db        756 ATWWATATATAWTTWTAWWWATWWAWWWTATAWATAWAATAWAAWAWAWATAAATAWATA 815

Qy        970 ACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAGCTCGTGTCATAATTGCTGAAG 1029
              : |:      |:| |::  : | || : || :   |||  |    |  :|||:    :|
Db        816 WATWAAAWAWAWATAWWATWATATAWWAATAWAWAAAAAATWTAATATWAATWATAAWAA 875

Qy       1030 AATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTTTGAAAAATCTCACCTTT 1089
              ||   |: :  :  :   |::| : |    |:  |  :|  :   |||||    |   :
Db        876 AAAATAWAWTTWWTWTTTTWWAWWATATAAAWAWATAWAAAWAAAAAAAAAAAAAATAAWA 935

Qy       1090 GAAAATAAATAAATTTATTTTAAATGCATATTTTATTAGTAATACTAACAATTGTAGGAA 1149
              :: :  | |:   |||  :|: || || : ||:: : : ||| | : | :| ||   :
Db        936 WWWTWATATTWTTATTAAAWTWTATWWATTWATTWWAWTWTATAWTTWTATWTATATATW 995

Qy       1150 ATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAAACAGTCTTAACAAAAAA 1209
              :| :  :||   ||  ||| ::  || ||| :||  | | | |   |   :: | | | |:
Db        996 WTAWTAWATATATTTATTAAWWTATATTTTAWAAAWTAATATATWATAWWWTAWATATAW 1055

Qy       1210 AAAAAAAAA 1218
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Db       1056 AWWAATTAW 1064


RESULT 3
CNS0039G
LOCUS       CNS0039G                1101 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL063921
VERSION     AL063921.1  GI:4941778
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:7227"
                     /clone="BACR08K10"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
ORIGIN

  Query Match             5.5%;  Score 66.8;  DB 9;  Length 1101;
  Best Local Similarity  18.5%;  Pred. No. 0.0043;
  Matches  126;  Conservative  273;  Mismatches  282;  Indels    1;  Gaps    1;

Qy         12 TAAATTTAAAAAACAAGCATTATGGGAGTTGATAAGACTTAAGAAGAAATTGTTCTTGAA 71
              :|||:  || ||  ::  : :|    | |: | || |   :|  | :  |  |:    ||
Db        417 WAAAWAAAATAATTWWAAWAWAAAAAATTWWAAAAWAAAAWAWTAWWTTTAWTWAAAAAA 476

Qy         72 AATAAACCCGAACTTCTCAACGAATACAAATTTATTTACAAGGATACTGAATATGACTGC 131
              || |||        || :       :| |::||:::||| |:  | |   || :  |
Db        477 AAAAAATTWTTTTTTTWTTTAWTTWATAWWTTWWWTTAAAWAAAAAAAAAAAWAAAWAAA 536

Qy        132 ACTGAATATGCTAAATCAAATAAGCATCCTGGCGGTCTTAATTTCCTCAATTTGTTTATT 191
              : | |||:|  |:: |:  : |:  |  :      ::|:  :|:::  :|:| |:: :|
Db        537 WATAAATWTWWTWWTTYTTWAAWATAAAMCMAAWYYHTYTTYTYHYYTYWTYTMTWHYHT 596

Qy        192 GATGAGAAGTAAGATTTGACTGAATATTTCAGAACACTCCATTCTAAGTAGGCTTTGAAA 251
              | | |: |:  :::| |:: ::|:::|:: :::: |: | :::    :  :::  :::
Db        597 MYTHAWAHTTWYHWYHTYAMWHWMTWHWTMWAWWHWTTYTAAYYYYYTCMYYYHYMHWHH 656

Qy        252 ATTTTAAAATCCTTCCCTAAGACTGGCGCAAAATAAGAGGAGACTGAATCTTCAAAGAGA 311
              |: : ||::| :|:  :  : | :  : ::  | :        ::    :::: |:: : :
Db        657 AHAHAAAWWTTHTWWTHAYHWATYHYYYYMYCAMMCMCTHTCHHCYYYYHHYTAHHTHTH 716

Qy        312 TTCTCAATATTAAAGAAAAAGCTTAAGCATTTATTCGAACCAAACTGGCCTATCGAAATT 371
              ::: :   :::::|  ::     | : ::::: ::  :    |: :   ::::   ||
Db        717 HWYAHYYMWYYMWAYYWMYCTACTYHYHHHHHYHWAYHTTWYAWAHAMWMWHHAHYAAAA 776

Qy        372 GGTTTATTCTTAACTACCTTTACTTTATTTGTCACTGGATGTTTGACTCA-AAAGTGGTA 430
                :|||:::: |:::::| ::::  :|  ::||   : ::: |:||: : : :  |:
Db        777 AWAAWATTHHYHHTTHYMHHTYMYHYYMYTCCYMCTYHCWHYYHTAYTCWTWTHHWMWTW 836

Qy        431 TTTCTCTATTCCCCTTCTTGTCTTAATGCAAATCATCAGTGGTTGGATTGGTCACTCTAT 490
              |:::::|::::   :: :: |:|: ::  :| |  :           :::   :::::::
Db        837 THWYHHTWWHHTTTHWAWWHTHTWCWWWWHATTWTWATHCWACMTMHWHHWMHMHHHHMA 896

Qy        491 GAACCACAATCGTAACCCTATATTAAGAAAATTCGCTTTAGTCTACGCTCCTCTTTGTGG 550
               :|::: :: : :::::|| :::: : ::  ::: : ::: :::::  :: |:||
Db        897 CHAHHHTHMCMCHHHMHCTCHHHHTMYHMTCHWMWHMHWHWHHWWMATWMTTMTTMMMMC 956

Qy        551 TGGTTTCTCTAATAAATGGTGGGGTAGGAAGCACAATCAACATCATATGTTCACAAACAA 610
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                ::::|::::: ::          |   :|  :::  |  :::| ::| :|   :|: |:
Db        957 CMMHHHCHMYHMMHMYMYCCHYYCTCHTHATTHYHYMCTCYHYCTWHTYWTAYWWAWTAH 1016

Qy        611 CATTCTAAAGGACGAAGATATCTAACACGATTACAAATTGTGGTAATTCCCCTTCTTATT 670
               :|| |:::  :  |: ||:: ::: :  |::||  ::: :  |: |:::::|:: :: :
Db       1017 AMTTATWWWWMHWWAHWATWWWWWWWWATAWWACTCHHWTWYHTHCTWYYHHTYHMWWAW 1076

Qy        671 TTTAAAGTGGAAATTAGACTCC 692
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Db       1077 WMAWHWHHMYAHYHWAHHCWYY 1098


RESULT 4
CNS0039G/c
LOCUS       CNS0039G                1101 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL063921
VERSION     AL063921.1  GI:4941778
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR08K10"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
ORIGIN

  Query Match             5.4%;  Score 65.8;  DB 9;  Length 1101;
  Best Local Similarity  16.6%;  Pred. No. 0.0068;
  Matches   97;  Conservative  250;  Mismatches  238;  Indels    0;  Gaps    0;

Qy        633 TAACACGATTACAAATTGTGGTAATTCCCCTTCTTATTTTTAAAGTGGAAATTAGACTCC 692
              ::: | :|: : :::  ||  || ::    :: |::|:::::::    | :||   :
Db       1067 DRRWAGDADRWAWDDGAGTWWTATWWWWWWWWATWDTWWDKWWWWATAAKTDTAWTWWRT 1008

Qy        693 ATCTTAGCTTCTTATTATGAATTTGAAGGAATCTTCCTTGCCTTGCACTGGGTATTATTA 752
              |:  ::   :    : : :|||: : ||:::   :  :::  ::| : ::||: ::| :|
Db       1007 AWRADWAGRDRGAGKRDRDAATDADGAGRRDGGRKRKDKKDRKDGDDDKKGGKKKKAAKA 948

Qy        753 TTCAACTAAAACTTCTATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTTCAGTGCT 812
               : |  ::::: :: :::::  :::  ::  |: ::: : :  :::|: |: :::: :
Db        947 AKWATKWWDDWDWDKDWKWDGAKDRKADDDDGAGDKDDDGKGKDADDDTDGTKDDDDKDK 888
```

```
Qy        813 TCTATTCTTGTTGGAAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCA 872
              : :::: :  : :  :|: ||:::::  |:|: : ::   ::: |::::: : ::::  :
Db        887 WDDWDKAKGTWGDATWAWAATDWWWWGWADADWWTWDAAADDWWADDRWDAWAWKWDDAW 828

Qy        873 TTTTTCGAACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTA 932
              :     :: :: ::|  :     :: :::|: ::   ::   |  :  : || | : ::
Db        827 AWGARTADRRDWGDRAGKRGGARKRRDRKRADDKRDAADDRDDAATWTTWTTTTTRDTDD 768

Qy        933 CTTATTATGGGTGGTATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTC 992
               :: |: : :   :  :: ::::: ::| |  : :    :  ::     ::: :  :|
Db        767 WKWKTDTWTRWAADRTWDRDDDDDRDRAGTAGRKWRRTWKRRWKRRDTRWDDADADDTAR 708

Qy        993 TACAGATTACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAG 1052
              :: ::: ::   |  | : | :  : :: |    :| :|: |::   :|: :: : :::
Db        707 DDRRRRGDDGADAGKGKKTGRKRRRRDRATWDRTDAWWADAAWWTTTDTDTDDWDKRDRR 648

Qy       1053 ATTCATGAAGGACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAA 1112
              ::  : :::  |   ::::|::|:::|: :     :  :::| : :|:|:: :::: :|:
Db        647 RKGARRRRRTTARAAWDWWTWKAWDWAKWDWKTRADRWDRWAADTWTDARKADRDWAKAR 588

Qy       1113 ATGCATATTTTATTAGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTA 1172
              |:: : :    |  :: : |  :   | :| :| :||:: :  :||   |: ||:  |:
Db        587 AWRARRDRARAARADRRWTTKGKTTTATWTTWAARAAWWAWWAWATTTATWTTTWTTTWT 528

Qy       1173 TTACTTTTTAATCTGAGAAAACAGTCTTAACAAAAAAAAAAAAAA 1217
              ||  ||||| :| | | ::|| :   : |: |||:|||||||:||
Db        527 TTTTTTTTTTWTTTAAWWWAAWWTATWAAWTAAAWAAAAAAAWAA 483


RESULT 5
CNS00DKY/c
LOCUS       CNS00DKY                928 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR27A24 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL071865
VERSION     AL071865.1  GI:4948170
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 928)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .928
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR27A24"
                     /clone_lib="RPCI-98"
                     /note="end : T7"
ORIGIN
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  Query Match             5.1%;  Score 62;  DB 9;  Length 928;
  Best Local Similarity   31.1%;  Pred. No. 0.039;
  Matches  122;  Conservative   86;  Mismatches  184;  Indels    0;  Gaps    0;

Qy        827 AAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCA 886
              |||  |  ||||  |||  |||    ||| || ||  |    |  |       || |  |
Db        922 AAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 863

Qy        887 AATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGG 946
              ||::     ||  : :::| :: :   :::: :::  |  ::::::::::: |   |
Db        862 AAWWYTCMAAAMAMAMMMCVMMMMMMMMMMMMMMTTMWWHHHWHHHHHHWTTTTTTTW 803

Qy        947 TATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAA 1006
              | | |  | ||  : : :: :: : ||:::   :::::::  |   : :  : :|   ::
Db        802 TTTTTTTTTTTTTWWWWWWWWWWWWTTTWWWWTWWWWWWWWWWTNNNWNMCHWAWATWWWW 743

Qy       1007 AGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACC 1066
              :  |  | : ||: :   | :| ||  ||| ||    ||  ||    || |:  :  |
Db        742 WWATATTTWTATWTWAWATAWAAAAAAAAAAAAAAWTAAATTTTTWTTTTAWTTWTAAAA 683

Qy       1067 TATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATT 1126
              | |||   :   | |   |:|  : ||| | :|:| :|:  :|:||      |: : |
Db        682 TTTTTTATTWTTTTTTWTTTWTTWTATATAAWAWTAWAWAAWAWATATTATATWAWAT 623

Qy       1127 AGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCT 1186
              | | ::  | : :  |  |  ::   : |||     : | :| |||  | |:   :|
Db        622 ATTTWWTATTWAWTATAAAATWWTAWWTTTAAWTAAWATAWAATTAAAAWTWAAAWAAAA 563

Qy       1187 GAGAAAACAGTCTTAACAAAAAAAAAAAAAAA 1218
                | |:|| |   || : :|||||::|||||:|
Db        562 AAAAWAAAATAWTTTWTWAAAAAWWAAAAAWA 531


RESULT 6
CNS00EPO/c
LOCUS       CNS00EPO                1101 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC:
            BACR29P01 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL069493
VERSION     AL069493.1  GI:4949636
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
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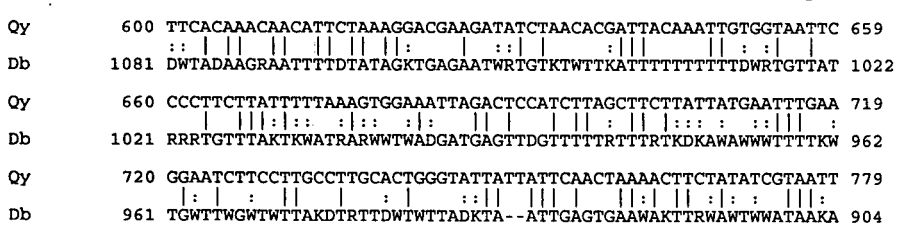
/db_xref="taxon:7227"
/clone="BACR29P01"
/clone_lib="RPCI-98"
/note="end : T7"

ORIGIN

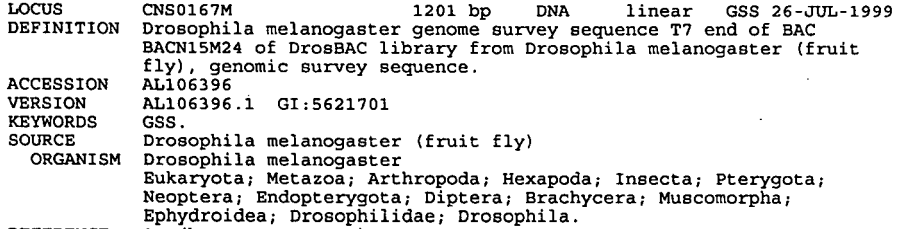
Query Match 5.1%; Score 61.8; DB 9; Length 1101;
Best Local Similarity 34.8%; Pred. No. 0.043;
Matches 207; Conservative 85; Mismatches 300; Indels 2; Gaps 1;



RESULT 7
CNS0167M/c
LOCUS CNS0167M 1201 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC BACN15M24 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL106396
VERSION AL106396.1 GI:5621701
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
FEATURES Location/Qualifiers
source 1. .1201
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN15M24"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : T7"

ORIGIN

Query Match 5.0%; Score 61.4; DB 9; Length 1201;
Best Local Similarity 39.1%; Pred. No. 0.051;
Matches 156; Conservative 40; Mismatches 203; Indels 0; Gaps 0;



RESULT 8
BH177277
LOCUS BH177277 886 bp DNA linear GSS 19-OCT-2001
DEFINITION 008_L_22-rev SmBAC1 Schistosoma mansoni genomic clone 008L22 5', genomic survey sequence.
ACCESSION BH177277
VERSION BH177277.1 GI:16275873
KEYWORDS GSS.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 886)
AUTHORS Le Paslier,M.C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W., Williams,D.L., Johnston,D., LoVerde,P.T. and Le Paslier,D.
TITLE Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library
JOURNAL Genomics 65 (2), 87-94 (2000)
MEDLINE 20247747
PUBMED 10783255
COMMENT Other_GSSs: 008_L_22-21
Contact: Pierce RJ
INSERM U 167

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           Institut Pasteur de Lille
           1 rue du Professeur A. Calmette, 59019-Lille, France
           Tel: (33) (0)3 20877783
           Fax: (33) (0)3 20877888
           Email: Raymond.Pierce@pasteur-lille.fr
           CNS sequencing ID=DG0AA008DF11BP1
           Plate: 008  row: L  column: 22
           Seq primer: M13 reverse primer
           Class: BAC ends
           High quality sequence stop: 886.
FEATURES             Location/Qualifiers
     source          1. .886
                     /organism="Schistosoma mansoni"
                     /mol_type="genomic DNA"
                     /strain="Puerto-Rican"
                     /db_xref="taxon:6183"
                     /clone="008L22"
                     /sex="mixed"
                     /dev_stage="cercariae"
                     /lab_host="Biomphalaria glabrata"
                     /clone_lib="SmBAC1"
                     /note="Vector: pBeloBAC 11; Site_1: Hind III; Partially
                     Hind III digested and size-selected S. mansoni  cercarial
                     DNA was ligated into Hind III digested pBeloBAC 11 vector
                     and used to transform E. coli DH10B. The complete library
                     contains 23808 clones from 4 independent
                     sizing-ligation-transformations.  Average insert size
                     ranges from 70-127 kb and genome coverage is 7.9-fold."
ORIGIN

  Query Match             5.0%;  Score 60.4;  DB 8;  Length 886;
  Best Local Similarity   39.9%;  Pred. No. 0.08;
  Matches  157;  Conservative   47;  Mismatches  183;  Indels    6;  Gaps    1;

Qy        827 AAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCA 886
              |||| :   | :  | || :| ||  | |     ||:   ||:::|||: |   | |
Db        416 AAATAMATYASMSNATATAVATTTAAATAATTTTATMTANTTMMMATTWATTATAAAMAT 475

Qy        887 AATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGG 946
              ::|: :  :||  :  ::: |      :::  |:: ||::| | | :| |  |:
Db        476 WWTMAMAAMAAMTMMTMMMMATYTMMMMHWAMAMMAATWMTTTTTTMTAAMAAWTTTATT 535

Qy        947 TATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAA 1006
              ||:  || :| | | : |  ||   |:  |   |  |: | |  ||  :       |
Db        536 TAWAAAAAWTAAWATWAATAATTTTTWAATTATAATAWATTWTAATTATTTWAATTATTA 595

Qy       1007 AGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACC 1066
              :  :  :  :|||||  | || ||  ||  :  |      |  | | :  | |   |
Db        596 WTTWATWAAAWTAATTTTTTAAAAAAAAATAWTTT------TATAAAAWTTTTATTAATW 649

Qy       1067 TATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATT 1126
              ||:|||  |||||| | |  ||  |||:| || || ||| |||:  |    |||| |
Db        650 TAWTTTAAAAAAATTTTAATTTATAAAWTTAAAAATTTTTTTTTWTTTAATAATTTAAAA 709

Qy       1127 AGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCT 1186
              | ||| | ||| |||| ||  |||    | ||  | |  :| |  :| ||   |:  :
Db        710 ATTAAAAATAAAAATTTTAAAAAAAAAWTAATAATNTAAWTTTTATAWAATTAAAAWAAW 769

Qy       1187 GAGAAAACAGTCTTAACAAAAAAAAAAAAAAA 1219
               |:||||   : | |  ||    ||||||||||
Db        770 AARAAAAWTAWTTAATAAATTTTAAAAAAAAA 802


RESULT 9
CNS07JUX
LOCUS       CNS07JUX                886 bp    DNA     linear   GSS 30-NOV-2001
DEFINITION  T3 end of clone 008DF11 of library SmBAC1 from strain Puerto-Rican
            of Schistosoma mansoni, genomic survey sequence.
ACCESSION   AL614235
VERSION     AL614235.1  GI:16027459
KEYWORDS    GSS.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 886)
  AUTHORS   Le Paslier,M.C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W.,
            Williams,D.L., Johnston,D., LoVerde,P.T. and Le Paslier,D.
  TITLE     Construction and characterization of a Schistosoma mansoni
            bacterial artificial chromosome library
  JOURNAL   Genomics 65 (2), 87-94 (2000)
  MEDLINE   20247247
   PUBMED   10783255
REFERENCE   2  (bases 1 to 886)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-OCT-2001) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Partially Hind III digested and size-selected S. mansoni cercarial
            DNA was ligated into Hind III digested pBeloBAC 11 vector and used
            to transform E. coli DH10B. The complete library contains 23808
            clones from 4 independent sizing-ligation-transformations. Average
            insert size ranges from 70-127 kb and genome coverage is 7.9-fold.
FEATURES             Location/Qualifiers
     source          1. .886
                     /organism="Schistosoma mansoni"
                     /mol_type="genomic DNA"
                     /strain="Puerto-Rican"
                     /db_xref="taxon:6183"
                     /clone="008DF11"
                     /clone_lib="SmBAC1"
                     /note="end : T3"
ORIGIN

  Query Match             5.0%;  Score 60.4;  DB 9;  Length 886;
  Best Local Similarity   39.9%;  Pred. No. 0.08;
  Matches  157;  Conservative   47;  Mismatches  183;  Indels    6;  Gaps    1;

Qy        827 AAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCA 886
              |||| :   | :  | || :| ||  | |     ||:   ||:::|||: |   | |
Db        416 AAATAMATYASMSNATATAVATTTAAATAATTTTATMTANTTMMMATTWATTATAAAMAT 475

Qy        887 AATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGG 946
              ::|: :  :||  :  ::: |      :::  |:: ||::| | | :| |  |:
Db        476 WWTMAMAAMAAMTMMTMMMMATYTMMMMHWAMAMMAATWMTTTTTTMTAAMAAWTTTATT 535

Qy        947 TATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAA 1006
              ||:  || :| | | : |  ||   |:  |   |  |: | |  ||  :       |
Db        536 TAWAAAAAWTAAWATWAATAATTTTTWAATTATAATAWATTWTAATTATTTWAATTATTA 595

Qy       1007 AGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACC 1066
              :  :  :  :|||||  | || ||  ||  :  |      |  | | :  | |   |
Db        596 WTTWATWAAAWTAATTTTTTAAAAAAAAATAWTTT------TATAAAAWTTTTATTAATW 649

Qy       1067 TATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATT 1126
              ||:|||  |||||| | |  ||  |||:| || || ||| |||:  |    |||| |
Db        650 TAWTTTAAAAAAATTTTAATTTATAAAWTTAAAAATTTTTTTTTWTTTAATAATTTAAAA 709

Qy       1127 AGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCT 1186
              | ||| | ||| |||| ||  |||    | ||  | |  :| |  :| ||   |:  :
Db        710 ATTAAAAATAAAAATTTTAAAAAAAAAWTAATAATNTAAWTTTTATAWAATTAAAAWAAW 769

Qy       1187 GAGAAAACAGTCTTAACAAAAAAAAAAAAAAA 1219
               |:||||   : | |  ||    ||||||||||
Db        770 AARAAAAWTAWTTAATAAATTTTAAAAAAAAA 802


RESULT 10
CNS008HI
LOCUS       CNS008HI                961 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR17O01 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL051882
VERSION     AL051882.1  GI:4933734
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KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 961)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .961
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR17O01"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
ORIGIN

  Query Match             5.0%;  Score 60.4;  DB 9;  Length 961;
  Best Local Similarity   39.4%;  Pred. No. 0.081;
  Matches  224;  Conservative   46;  Mismatches  290;  Indels    8;  Gaps    1;

Qy        647 ATTGTGGTAATTCCCCTTCTTATTTTTAAAGTGGAAATTAGACTCCATCTTAGCTTCTTA 706
              :|| |  |  ||    || || |||| ||||  |   ||  | |      ||  |  |||
Db         13 DTTTTTTTTTTTTATNTTTTTTTTTTAAAAGAAGCKKTTTCAATGACCGTTGNCGGCTTT 72

Qy        707 TTATGAATTTGAAGGAATCTTCCTTGCCTTGCACTGGGTATTATTATTCAACTAAAACTT 766
              ||:| | ||| :|    |     || | ||  : |     |||::|||  | | :   |
Db         73 TTWTAATTTTWWATATTTAACATTTTCGTTAAWTTTTAATTTAWWATTTTATTTWTTWTG 132

Qy        767 CTATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTGG 826
              :| |    ||| ||  |  :||  ||  :  ||| ||   |     ||      |
Db        133 TCWTCTWTATATTATTAATWTWTTTTTTTKWTTTTTTTTTTTTTTAACTTACATACATATA 192

Qy        827 AAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCA 886
              | |  | ||||  ||   | ||  | | ||   |   ||    ||||||  |
Db        193 TATTTCTTTAAATAGAAAATACTTTTATAAAATTTTTTTTTATAAATTTTTAAATTTATT 252

Qy        887 AATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGG 946
              | ||  |       | |:|    | |          || | | ||||||||||:  |
Db        253 ATTATTTTTTTTATTATAYTTKTWTAT--------ATTTTTTTWTACTTATTATKAATAT 304

Qy        947 TATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAA 1006
              ||| || | : | : : :  || : |||||    |:||||  ||:      :|:
Db        305 TATATATTTWCATWTWTWTTATTWTTTTTTATTTTWAATTTTTTWTATTKTWTWCTTATT 364

Qy       1007 AGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACC 1066
               : :  | | |:| |:  |  |    ||         :|   |:   :|  |     :
Db        365 TKWWTTTWTTAWATTKTTTWTAATYATATTTGTTAATWATAATWTTTWTKTTATTTTWWT 424

Qy       1067 TATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATT 1126
              | ||||| ||:|||| ||  :| :  || : |: :||: ||||      ||||:||  :
Db        425 TTTTTTTTAAWAATCATACAAWTTWTTATTWTTWTWTTKTTTTTTTTATTATATKTTTAY 484

Qy       1127 AGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCT 1186
              |  |  :|  | || ||   | : | |  |  | | ||   |: :|: |:  |  | |
Db        485 TTTTTTTTWATAATTTTTATATATKTTTTATTAATATTTTATATYTWTWGTWAATTTTTT 544

Qy       1187 GAGAAAACAGTCTTAACAAAAAAAAAAA 1214
                :| :   |||  ||| | |||||
Db        545 TTATTWATWTATTTATAAAATAGAAAAA 572


RESULT 11
CNS00EVL/c
LOCUS       CNS00EVL                1101 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC:
            BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL069706
VERSION     AL069706.1  GI:4949849
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR29B23"
                     /clone_lib="RPCI-98"
                     /note="end : T7"
ORIGIN

  Query Match             4.9%;  Score 60.2;  DB 9;  Length 1101;
  Best Local Similarity   33.0%;  Pred. No. 0.089;
  Matches  181;  Conservative   92;  Mismatches  275;  Indels    1;  Gaps    1;

Qy        666 TTATTTTTAAAGTGGAAATTAGACTCCATCTTAGCTTCTTATTATGAATTTGAAGGAATC 725
              | :|||:|||| |  |::|||      || |:   |  :   ||| :|| : |:   |:
Db       1033 TAWTTTWTAAAATATAWWTTAATAAATATATWTAWTAWWATATATAWATAWAAWTATAWA 974

Qy        726 TTCCTTGCCTTGCACTGGGTATTATTATTCAACTAAAACTTCTATATCGTAATTCTTTCT 785
              :|       |  |     | | || |:   | :|::: :|   | |  |  || |:| |
Db        973 WTWWAATWAATWWATAWAWTTTAATAAWAATATWAWWWTWTTATTTTTTTTTTTTTWTTT 914

Qy        786 GAATTGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTGGAAATCATGAAAATGAAATG 845
              ||: :||  |  ::|| :  | :  :  : :| || ||    || || :| || |:||
Db        913 WTATWTWTTTATATWWTWWAAAAWAWWAAWTWTATTTTTTWTTATWATTWATATTAWATT 854

Qy        846 AAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCAAATAGCTGCAAGCAGAAAC 905
              |:   |  :: |   : |::  :|:|:|  :| :| | :||  |  :   :  :
Db        853 TTTTWTWTATTWWTATATWATWWTATWTWTWTTTWATWT-ATWTATTTATWTWTWTTWTA 795
```

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Qy        906 TACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGGTATGTAATATTAGACTGAA 965
              |    |:|  |  : ::||: :    | |   |||   |  ||| : :  |:  : |  |
Db        794 TTWTATWTATAWWWTWWATWWWTAWAAWTATATATWWATATTATWWTWATTWTTWTTTTA 735

Qy        966 CATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAGCTCGTGTCATAATTGCT 1025
                :   |  :|   :|| : |  ||: |:    ||         :  | | | | |   |
Db        734 TTWTTTTAAWTTATWTATWATTWTTWATWTTTTTTTTTTTTTTTWTATTTWAAATTATTT 675

Qy       1026 GAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTTTGAAAAATCTCAC 1085
              |  |:::||  |: |       | |: | | |           | ||||  :|||    |
Db        674 AATTAWWWAATWAWTTATTTAATAAWTAATTAAATTATTAAAAATTTTATWAAAAAATAT 615

Qy       1086 CTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTAGTAATACTAACAATTGTA 1145
              |||  | || |||:|: ||  | :|     |||::||:| | | :|    : | |: |
Db        614 TTTTTTATATTAATWAWATTTATAWATTAATATAWWTTWTAAATTWTTAATWTATTWWTT 555

Qy       1146 GGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAAACAGTCTTAACAA 1205
                || | | || |  ||| :| : :: : | :  |:|:: : | |||  : : :|    :
Db        554 TAAATTATWTTTTTTTTTAWTAWAWWTWAAAWAATWAWWWWWAAAAATWWWWTWTTTTTW 495

Qy       1206 AAAAAAAAA 1214
              |  :| ||:
Db        494 ATTWATAAW 486
```

RESULT 12
CNS001FB/c
LOCUS CNS001FB 1101 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR04A23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL060732
VERSION AL060732.1 GI:4939397
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES Location/Qualifiers
source 1. .1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR04A23"
/clone_lib="RPCI-98"
/note="end : TET3"
ORIGIN

Query Match 4.9%; Score 60; DB 9; Length 1101;
Best Local Similarity 38.7%; Pred. No. 0.097;

Matches 152; Conservative 58; Mismatches 180; Indels 3; Gaps 2;

```
Qy        827 AAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCA 886
              :::  || || |  | || ||||:  |:| || ||  |   ||  | |: |  || || |
Db       1072 WWWAAATWAATAAAATATWAAATWATAWATAATAAAAAAAATATAAATWATTAAAAATAA 1013

Qy        887 AATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGG 946
              |||:  |  ||  | :|| :|      |  |  |  ||:| | |  |    |  |:
Db       1012 AATW--TAAAAAWATWAAAWAAAAAATTWAATAATTAWTATATTNAAAAAAAAWAAAAAA 955

Qy        947 TATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAA 1006
              |  ||||| :: |   || |  |   |     |||||::   |:  | : |||:   ||
Db        954 AAATTAATAAWWAAAAAAAAAAWATAATAATATATAAAWWTAATWTAATWNATTWAAAAA 895

Qy       1007 AGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACC 1066
              |      :  |::|      :| || ||:| :|    :   :: | | :  | ||  |
Db        894 ATAATAWAATAWWAAATTAAWAAAAATAWATWAAAAAWNTAWWTATAAW-TTWAAAAATW 836

Qy       1067 TATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATT 1126
              | |: :: |||||| :    ||   | ||| :||| :| ||:|::||   | || : |:
Db        835 TNTWAWWWAAAAATWWTTTTTTAATATATATWTAATWTWWAAAAAAAATAWAAWA 776

Qy       1127 AGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCT 1186
              :  ::|: ::: |:   :|   ||| | : |       ||:| :   |: :|::: |
Db        775 WTAWWTWAWWWNAWAAAWAAATAATATAWNAAWAAAAATTWAWWANATWWWTWWWTAAAA 716

Qy       1187 GAGAAAACAGTCTTAACAAAAAAAAAAAAAAA 1219
              | |||| |    :|  || ||:||||||||||
Db        715 TAAAAAAAAAATAWATAAATAAWAAAAAAAAA 683
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RESULT 13
CNS04D0K
LOCUS CNS04D0K 945 bp DNA linear GSS 01-SEP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 101H21 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION AL285149
VERSION AL285149.1 GI:8023560
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE 1
AUTHORS Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296633
PUBMED 10835645
REFERENCE 2
AUTHORS Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
PUBMED 10899143
REFERENCE 3 (bases 1 to 945)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at

```
          http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .945
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="101H21"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG101CD11LP1~end : T7"
ORIGIN

  Query Match             4.9%;  Score 59.8;  DB 9;  Length 945;
  Best Local Similarity   40.1%;  Pred. No. 0.11;
  Matches  174;  Conservative   48;  Mismatches  209;  Indels    3;  Gaps    2;

Qy        789 TTGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTGGAAATCATGAAAATGAAATGAAA 848
              |:  ||  |  |      :: |  :: |:|| || ||  || | || |||:| ||| |
Db        433 TWNTTTTTTTTTTANTANYWTTAWWWTTWTTTTTTTTATAATTAATAAAAWTTAAANWATT 492

Qy        849 TTCGAAAGAAGAAT--CACTTTACCATTTTTCGAACATCAAATAGCTGCAAGCAGAAACT 906
              :|  ||| |: |||    |  | |  :::|||  || |  |:|||      |      |: :
Db        493 WTWAAAAWAWAAATAAAAAATAAWAWWWTTTTTAAAAAAAWATAATAAWATTWTWTAWAW 552

Qy        907 ACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGGTATGTAATATTAGACTGAAC 966
              :   ||:  |     ||||   :     ||| |    |  ||   |: | ||    | ||
Db        553 WATTTTWATATTTTTTATTTAAWAATAATATAAAAAATTTTAAAAAWAAATATTTTTAAW 612

Qy        967 ATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAGCTCGTGTCATA-ATTGCT 1025
              |  |  : |   ||||||   ||| || | : :|   |::  :  :   ::: |:
Db        613 AATAAAWATAAAAATAAATATATTTATAWAAWAWATAWAWWWWWTAWWAAWWWTAWAATA 672

Qy       1026 GAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTTTGAAAAATCTCAC 1085
              || || |||| :|    ||   ||| ||  |  :|  :   |::|:  ||:|     |
Db        673 TAAAAAATAAAAWAWAATAAAAATAAAATAAAAAWAAAWWAAAWWTWATAAWANAAAAAA 732

Qy       1086 CTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTAGTAATACTAACAATTGTA 1145
              |  | |  |: |||| ||  ||||||  | | | :||:: |||    || |||| :
Db        733 AAATATATAATAWAAAATATAAATTAAATATAAAATAWATWWATAAATAAAAAAATTTWT 792

Qy       1146 GGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAAACAGTCTTAACAA 1205
              |||     :       ||| :||||| : |  ||  |   |:  : |  ||| |
Db        793 AATAATAAAAAWATTAAAWATTATWTATTANWATAAAANTTATAAWNTAWNTAATAAATA 852

Qy       1206 AAAAAAAAAAAAA 1219
              ||| : ||||||||
Db        853 AAATWTAAAAAAAA 866


RESULT 14
CNS00KAE/c
LOCUS       CNS00KAE               1101 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR39P05 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL077628
VERSION     AL077628.1  GI:4956903
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR39P05"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
ORIGIN

  Query Match             4.9%;  Score 59.2;  DB 9;  Length 1101;
  Best Local Similarity   38.1%;  Pred. No. 0.14;
  Matches  216;  Conservative   20;  Mismatches  330;  Indels    1;  Gaps    1;

Qy        654 TAATTCCCCTTCTTATTTTTAAAGTGGAAATTAGACTCCATCTTAGCTTCTTATTATGAA 713
              | :|:    :| |::||| |||: |   | |:    |  || |:    | |||  ||  |
Db        579 TTWTWTTWTWTTTWWTTTATAAWTTTNTATTWTWTATTAATTTWTTAATTTTAAAATTTA 520

Qy        714 TTTGAAGGAATCTTCCTTGCCTTGCACTGGGTATTATTATTCAACTAAAACTTCTA-TAT 772
              |||      :| ||  |    ||    :  ||||||||    : : ||| |  || |||
Db        519 TTTTNTATTWTWTTWTTATWTTTTATTWATATATTATTAAATTWTWTAAAATAATATTAT 460

Qy        773 CGTAATTCTTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTGGAAATCA 832
              |    ||   | |  ||| |||     ||| ||      ||   || |  ||   || |
Db        459 TTATTTTAAATATATATTWATTTTATATTTATTATTATATTTATTTTTATTTWATTATTA 400

Qy        833 TGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCAAATAGC 892
              |    |  | |  |||||       | ||  |   |    :||||  |: |   |||
Db        399 TTTTTAATATAATAAATTTTTTNATATAAATAWAATTTTTWTTTTWAAWTAATTAATTTA 340

Qy        893 TGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGGTATGTA 952
              |    |    | | ||    ||  |  |    || | | || | || ||       | | ||
Db        339 TTATAATTTATAATATATATTATATTATTATTTTTTTATAATAATAATWCWCTATNTNTA 280

Qy        953 ATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAGCTCG 1012
              ||||  | |   ||  | | :    |  |      | | || |    |
Db        279 NTATTTNANTNTNTATATNTNTNWNTATATATATATNANWNANANATNANANTATATNTA 220

Qy       1013 TGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTT 1072
              | | : |  ||  | | |  |      |  |  |      |  |       || |
Db        219 TATNWNWNTCWCTATANANTANANANTNTTATATATNTNANTNTNTATNTANTATANTNA 160

Qy       1073 TGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTAGTAAT 1132
              |  |  ||   :  |   | ||  ||| | | |    ||       | | |   ||
Db        159 TATATNATAANWNTNTNTNANATNTATATANTNANANNAATATATATATATCTATATAGA 100

Qy       1133 ACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAA 1192
              |    || ||   :  | |      ||  |    |||   | | |||  |    |
Db         99 NAGANTTTTTATATANWNANTNTANANANTTTATANTNTATANATATNTAAATTATATAT 40

Qy       1193 ACAGTCTTAACAAAAAAAAAAAAAAAA 1219
              |      | || ||||||| || ||||:
Db         39 AATAATTAAATAAAAAAATAATAAAAW 13


RESULT 15
AG376784
LOCUS       AG376784               1324 bp    DNA     linear   GSS 03-JUN-2004
DEFINITION  Mus musculus molossinus DNA, clone:MSMg01-184I09.T7, genomic survey
            sequence.
ACCESSION   AG376784
VERSION     AG376784.1  GI:47987989
KEYWORDS    GSS.
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SOURCE      Mus musculus molossinus
  ORGANISM  Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     BAC end Sequences of Library MSMg01
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1324)
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institude, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
            PRIMERS
            Sequencing : T7
            LIBRARY
            Vector     : pBACe3.6
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            R.Site 2   : EcoRI.
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ORIGIN

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  Matches  258;  Conservative    0;  Mismatches  316;  Indels    5;  Gaps    1;

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Qy        682 AATTAGACTCCATCTTAGCTTCTTATTATGAATTTGAAGGAATCTTCCTTGCCTTGCACT 741
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Qy        742 GGGTATTATTATTCAACTAAAACTTCTATATCGTAATTCTTTCTGAATTGATTGCTGGTT 801
                | ||  |  ||  | | ||  |  ||  |  | ||| ||| |    | | |  |  ||
Db        592 ATTTTTTTTATTTTTATTTAATTTATTAATTTTTTATTATTTTTTTTTATTAATTTTTTTT 651

Qy        802 TCTTCAGTGCTTCTATTCTTGTTGGAAATCATGAAAATGAAATGAAATTCGAAAGAAGAA 861
              | |    |  || |||| || ||        |   |||   | |||||  ||   | |
Db        652 TTTATTTTTTTTTTATTATTTTTTTTTTTATTTTTTAATTTTTTTAAATTATAATTTATAT 711

Qy        862 TCACTTTACCATTTTTCGAACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACA 921
              |    |||   |||||  |  ||  |||   |  |   | |   ||   | |
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Qy        922 TATTCTCTCTACTTATTATGGGTGGTATGTAATATTAGACTGAACATCACTTTTTCCCAT 981
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Db        772 TTTTTTTTTAATTTTTATTATTTTATATTTATATTTATTTTTATATTTAATTAATTATTT 831

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Qy       1102 ATTTATTTTAAATGCATATTTTATTAGTAATACTAACAATTGTAGGAAATGTGTTATGGT 1161
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Job time : 4409 secs
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GenCore version 5.1.6


OM nucleic - nucleic search, using sw model

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(without alignments)
9252.626 Million cell updates/sec

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Perfect score: 1219
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| | 1 | 59 | 4.8 | 8056 | 18 | US-10-473-126-386 | Sequence 386, App |
| c | 2 | 58 | 4.8 | 6103 | 15 | US-10-311-455-1663 | Sequence 1663, Ap |
| c | 3 | 57.4 | 4.7 | 8056 | 18 | US-10-473-126-240 | Sequence 240, App |
| c | 4 | 54.6 | 4.5 | 8056 | 18 | US-10-473-126-386 | Sequence 386, App |
| | 5 | 53.2 | 4.4 | 1501 | 18 | US-10-473-126-328 | Sequence 328, App |
| | 6 | 52 | 4.3 | 640681 | 9 | US-09-790-988-1 | Sequence 1, Appli |
| c | 7 | 51.8 | 4.2 | 424 | 9 | US-09-960-352-11218 | Sequence 11218, A |
| c | 8 | 51.8 | 4.2 | 7319 | 15 | US-10-311-455-2017 | Sequence 2017, Ap |
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| | 15 | 50 | 4.1 | 16439 | 15 | US-10-311-455-860 | Sequence 860, App |
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| c | 32 | 47.4 | 3.9 | 17421 | 14 | US-10-239-676-54 | Sequence 54, Appl |
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| c | 34 | 47.4 | 3.9 | 19634 | 18 | US-10-473-126-302 | Sequence 302, App |
| c | 35 | 47.2 | 3.9 | 397 | 14 | US-10-198-846-1348 | Sequence 1348, Ap |
| c | 36 | 47.2 | 3.9 | 6749 | 16 | US-10-221-714A-247 | Sequence 247, App |
| c | 37 | 47.2 | 3.9 | 17703 | 16 | US-10-257-166-34 | Sequence 34, Appl |
| c | 38 | 47 | 3.9 | 6816 | 18 | US-10-723-860-7676 | Sequence 7676, Ap |
| c | 39 | 47 | 3.9 | 18988 | 15 | US-10-311-455-674 | Sequence 674, App |
| c | 40 | 47 | 3.9 | 18988 | 15 | US-10-240-485-62 | Sequence 62, Appl |
| c | 41 | 47 | 3.9 | 18988 | 16 | US-10-221-714A-64 | Sequence 64, Appl |
| c | 42 | 46.8 | 3.8 | 83391 | 17 | US-10-433-793-124 | Sequence 124, App |
| | 43 | 46.8 | 3.8 | 102980 | 13 | US-10-087-192-1330 | Sequence 1330, Ap |
| c | 44 | 46.6 | 3.8 | 5163 | 15 | US-10-311-455-1222 | Sequence 1222, Ap |
| c | 45 | 46.6 | 3.8 | 15373 | 15 | US-10-311-455-440 | Sequence 440, App |

ALIGNMENTS

RESULT 1
US-10-473-126-386
; Sequence 386, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 386
; LENGTH: 8056
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-386

Query Match 4.8%; Score 59; DB 18; Length 8056;
Best Local Similarity 44.3%; Pred. No. 0.06;
Matches 483; Conservative 0; Mismatches 585; Indels 23; Gaps 5;

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Qy       221 CAGA-----ACACTCCATTCTAAGTAGGCTTTGAAAATTTTAAAATCCTTCCCTAAGACT 275
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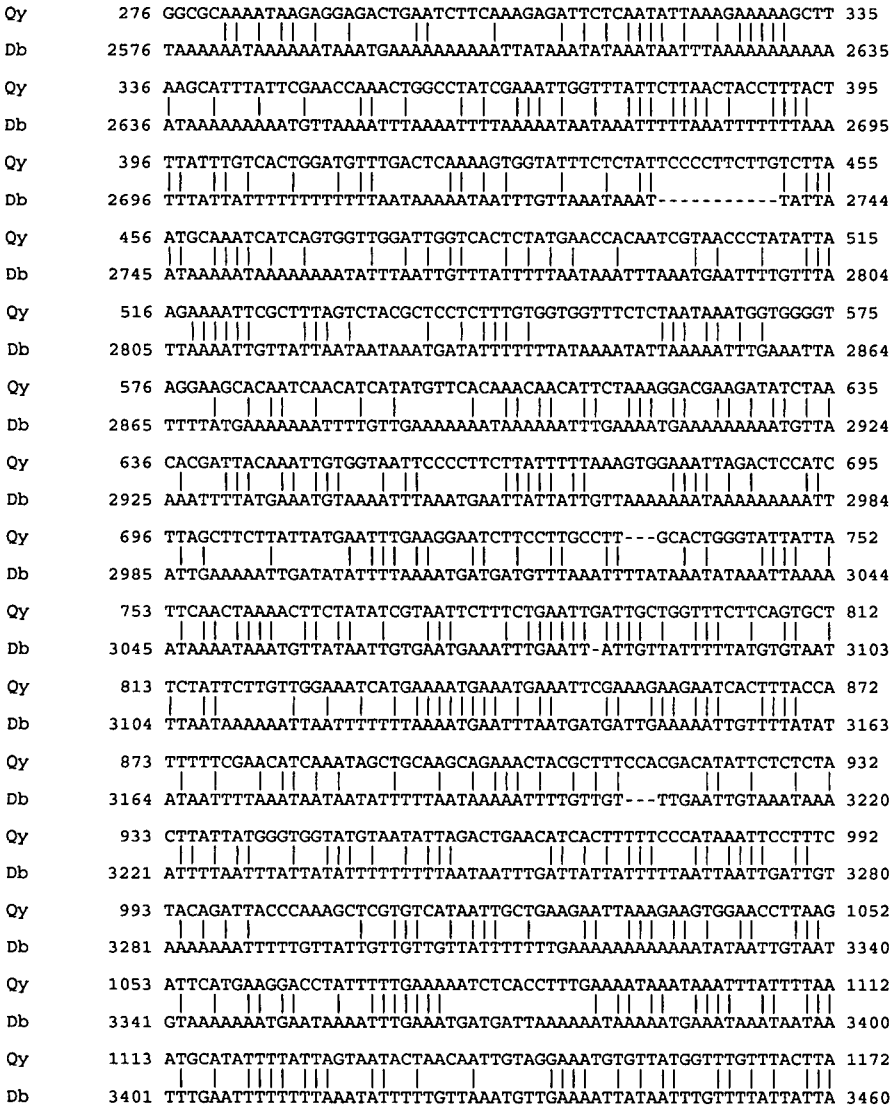

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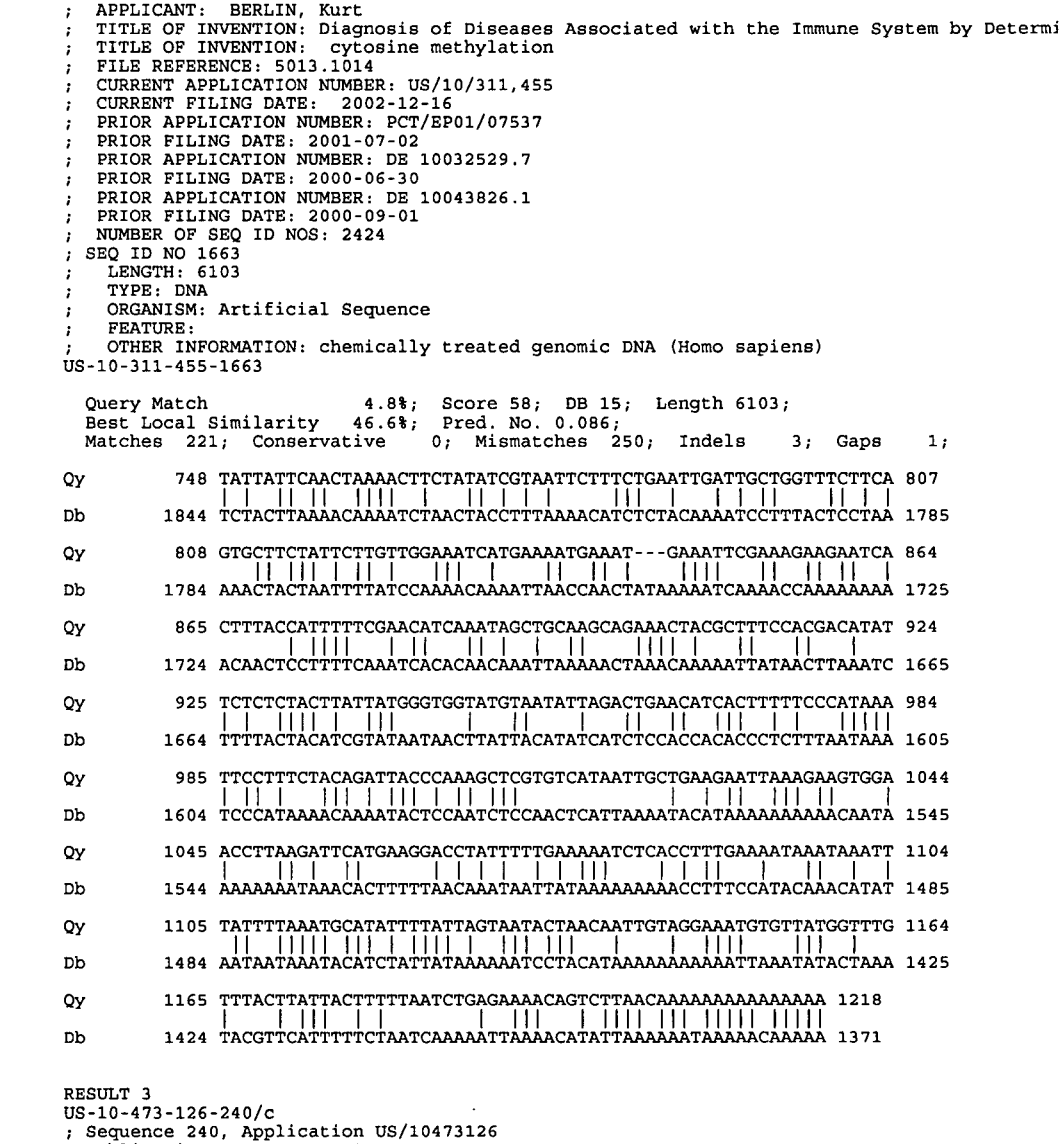
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian



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; Publication No. US20040234973A1
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; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 240
; LENGTH: 8056
; TYPE: DNA

;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-240

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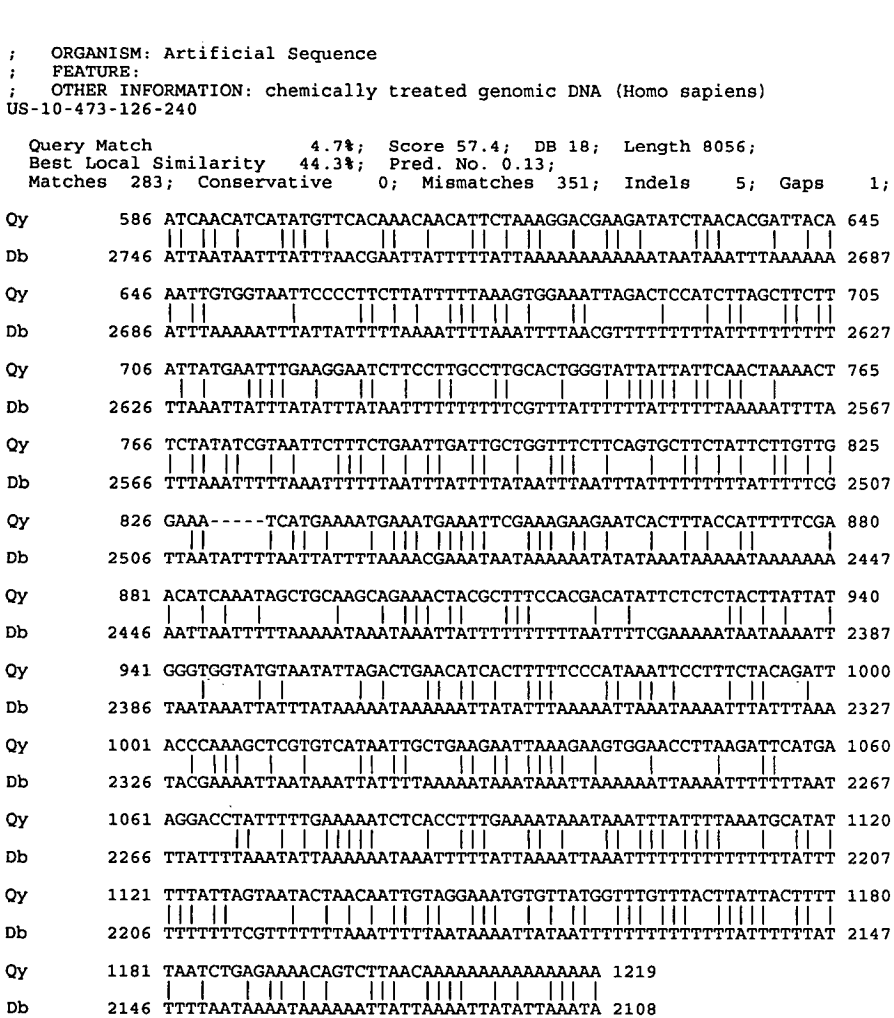

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; Publication No. US20040234973A1
; GENERAL INFORMATION:
;  APPLICANT: Epigenomics AG
;  TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
;  TITLE OF INVENTION: proliferative disorders
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/473,126
;  CURRENT FILING DATE: 2003-09-26
;  NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 386
;  LENGTH: 8056
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-386

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Best Local Similarity 45.3%; Pred. No. 0.5;
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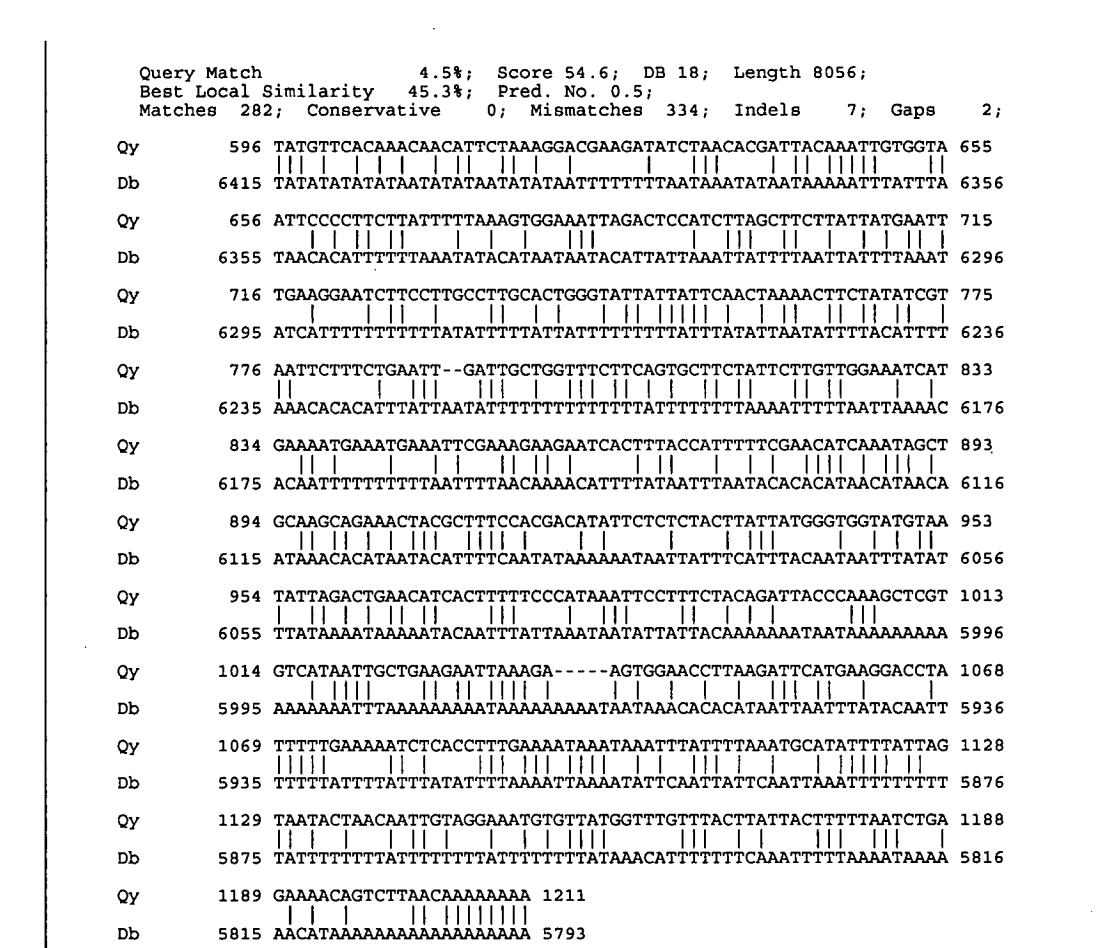

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; GENERAL INFORMATION:
;  APPLICANT: Epigenomics AG
;  TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
;  TITLE OF INVENTION: proliferative disorders
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/473,126
;  CURRENT FILING DATE: 2003-09-26
;  NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 328
;  LENGTH: 1501
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-328

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Best Local Similarity 46.1%; Pred. No. 0.49;
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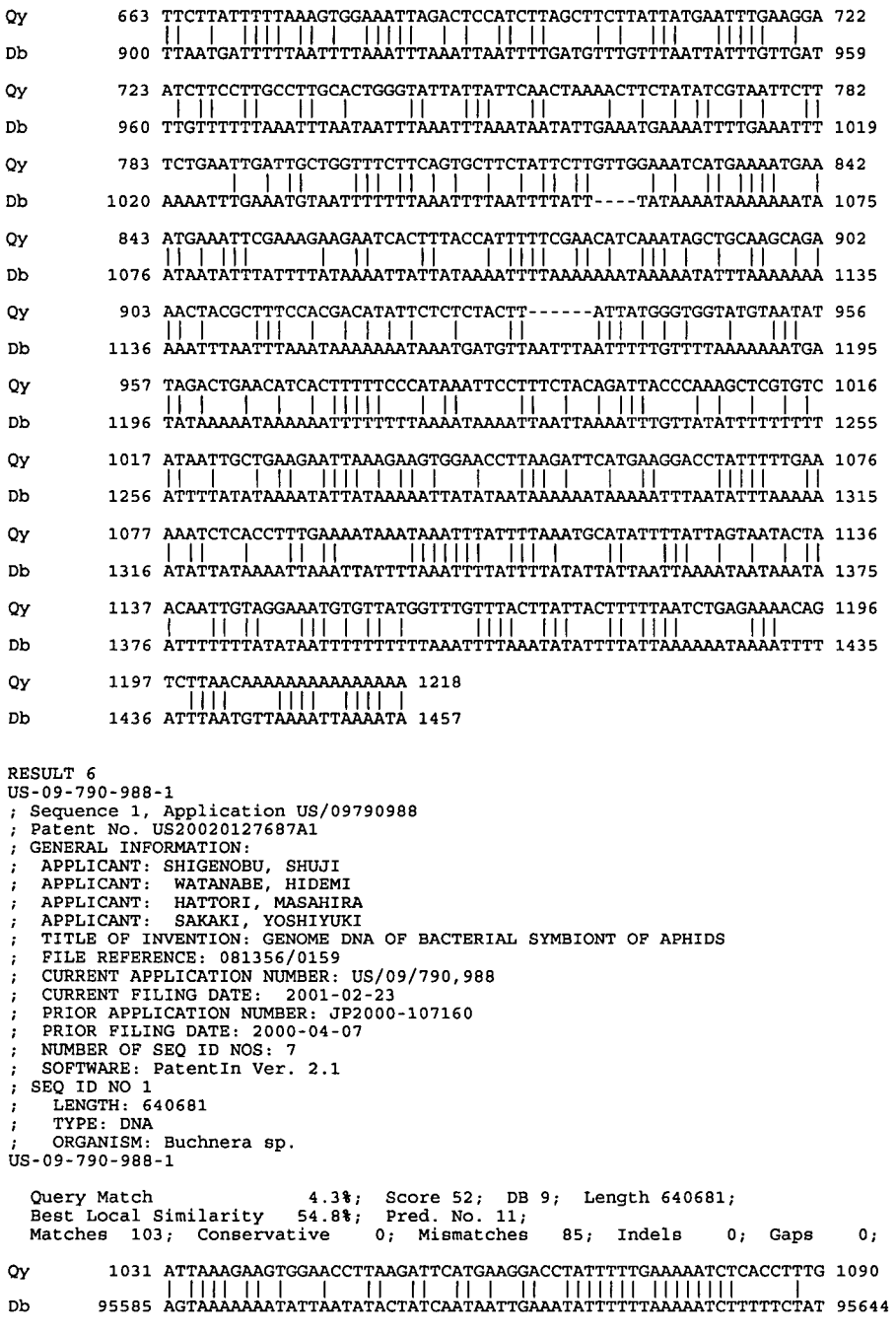

RESULT 6
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. US20020127687A1
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 4.3%; Score 52; DB 9; Length 640681;
Best Local Similarity 54.8%; Pred. No. 11;
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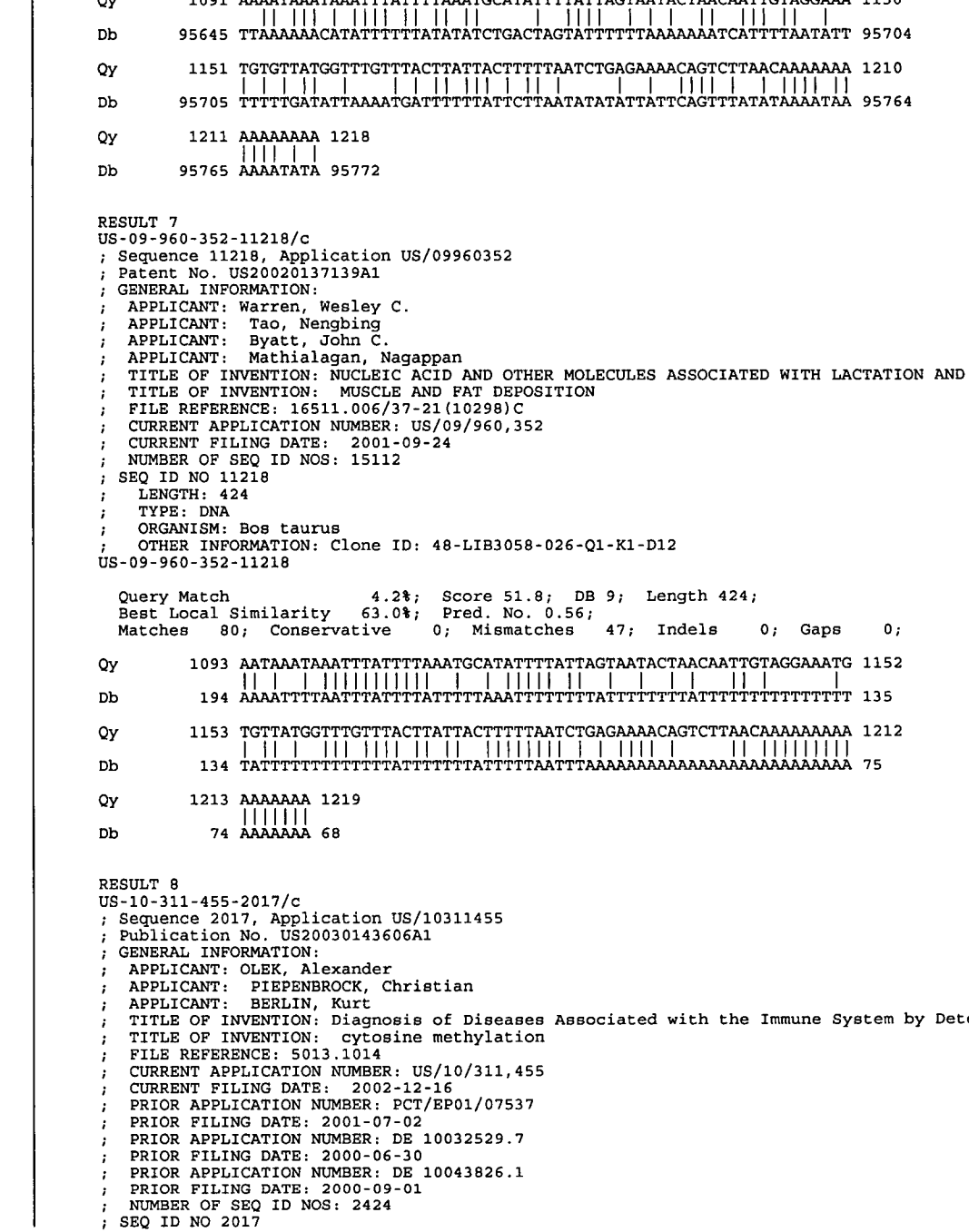

RESULT 7
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; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11218
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 48-LIB3058-026-Q1-K1-D12
US-09-960-352-11218

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; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determi
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 2017

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;   LENGTH: 7319
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-2017

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RESULT 9
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; Publication No. US20030143606A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
;  TITLE OF INVENTION:  cytosine methylation
;  FILE REFERENCE: 5013.1014
;  CURRENT APPLICATION NUMBER: US/10/311,455
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: PCT/EP01/07537
;  PRIOR FILING DATE: 2001-07-02
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 74
;   LENGTH: 5728
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-74

  Query Match             4.2%;  Score 51.4;  DB 15;  Length 5728;
  Best Local Similarity   54.7%;  Pred. No. 2;
  Matches  123;  Conservative    0;  Mismatches  101;  Indels    1;  Gaps    1;

Qy         989 TTTCTACAGATTACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCT 1048
               | |  ||  |  | | |||   | | ||| ||      || ||  ||| ||       |
Db        2910 TCTAAACGAAAAAACGAAACTCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAAATTCTTT 2851

Qy        1049 TAAGATTCATGAAGGACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATT 1108
               |||  ||||| ||     | ||      ||| |||  | || || ||||| ||||  |||
Db        2850 TAAATTTCATCAATTTTATTTTAAAACTAAAACTCTTCATTAAATATAAAAAAATCAATT 2791

Qy        1109 TTAAATGCATATTTTATTAGTA-ATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTT 1167
                ||||   ||||  || |  | | | | | |||| |   |||| | ||    |||
Db        2790 CAAAATTTCTATTCAATCATAATAAATTTAAAATTTTTTTAAATTTCTTTATATTTAACA 2731

Qy        1168 ACTTATTACTTTTTAATCTGAGAAAACAGTCTTAACAAAAAAAAA 1212
               |  |||||| || |||| | | || | |  || || |||  || |
Db        2730 ATATATTACATTATAATATTATAATAAAAACTAAATAAACTAATA 2686


RESULT 10
US-10-311-455-1982/c
; Sequence 1982, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
;  TITLE OF INVENTION:  cytosine methylation
;  FILE REFERENCE: 5013.1014
;  CURRENT APPLICATION NUMBER: US/10/311,455
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: PCT/EP01/07537
;  PRIOR FILING DATE: 2001-07-02
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1982
;   LENGTH: 5750
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1982

  Query Match             4.2%;  Score 51.2;  DB 15;  Length 5750;
  Best Local Similarity   45.7%;  Pred. No. 2.3;
  Matches  179;  Conservative    0;  Mismatches  213;  Indels    0;  Gaps    0;

Qy         827 AAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCA 886
               ||||  | ||||| |||  ||   |  | |      |          || |||| ||||  |
Db        4820 AAATATTTAAAATAAAAATAACGACACTAAATCTTAAAAAAATAAATCTTTCAAACAAAA 4761

Qy         887 AATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGG 946
               || |  |  || ||  || ||  |      |  | ||   ||||  | |
Db        4760 AACAAATATAAACAATAAATATCCCACGAAAAAAATTCCCTCTAAAATACGCCCTAAAAA 4701

Qy         947 TATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAA 1006
               | | || | ||   |  | |  |||| ||   | || || || | |  | ||  | |
Db        4700 AACGAAAAAATATTTTATAAAAAACTTATTTTAAAAACTTTCTCTTTCTAAATATCTCCT 4641

Qy        1007 AGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACC 1066
                 || | |   || |  | ||   || |      |  ||||| || ||   | |
Db        4640 TTATCCTATTTAAAATTATTAAACCTTCATACTATTTAACCTCAAAATATTTAACTACTT 4581

Qy        1067 TATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATT 1126
               |  | |  |||||   |||| | |  |   | ||    ||  |  |   | ||   ||
Db        4580 AAAATATTCAAAATTAAACCTATAATCAATCAAAATAAAATAAAATCTATTTCTTAATTT 4521

Qy        1127 AGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCT 1186
               | | ||      | || |     || |  | |  ||  ||   || |||   |  |||||
Db        4520 ATTTATTTATTTATTTTTTTTTATTTTATTTATTTATTTATTTTTTTAAAATAAAATCT 4461

Qy        1187 GAGAAAACAGTCTTAACAAAAAAAAAAAAAA 1218
                    | | |  ||| |||| | || || |
Db        4460 CGCCCTATCGCCCAAACTAAAATACAATAACA 4429
```

```
RESULT 11
US-10-221-714A-434/c
; Sequence 434, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with
;  TITLE OF INVENTION:  tumor suppressor genes and oncogenes
;  FILE REFERENCE: 5013.1005
;  CURRENT APPLICATION NUMBER: US/10/221,714A
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: PCT/EP01/02955
;  PRIOR FILING DATE: 2001-03-15
;  PRIOR APPLICATION NUMBER: DE 10013847.0
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: DE 10019058.8
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 434
;   LENGTH: 5750
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-434

  Query Match             4.2%;  Score 51.2;  DB 16;  Length 5750;
  Best Local Similarity   45.7%;  Pred. No. 2.3;
  Matches  179;  Conservative    0;  Mismatches  213;  Indels    0;  Gaps    0;

Qy        827 AAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCA 886
              ||||  | |||||  |||  ||   |   | |      |         || |||| ||||  |
Db       4820 AAATATTTAAAATAAAAATAACGACACTAAATCTTAAAAAAATAAATCTTTCAAACAAAA 4761

Qy        887 AATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGG 946
              || |  |  || ||  || ||  |      |  | ||   |||| | |
Db       4760 AACAAATATAAACAATAAATATCCCACGAAAAAAATTCCCTCTAAAATACGCCCTAAAAA 4701

Qy        947 TATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAA 1006
              | | || | ||   |  | |  |||| ||   | || || || | |  | ||  | |
Db       4700 AACGAAAAAATATTTTATAAAAAACTTATTTTAAAAACTTTCTCTTTCTAAATATCTCCT 4641

Qy       1007 AGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACC 1066
                || | |   || |  | ||  || |      | ||||| || ||   | |
Db       4640 TTATCCTATTTAAAATTATTAAACCTTCATACTATTTAACCTCAAAATATTTAACTACTT 4581

Qy       1067 TATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATT 1126
               |  | |  |||||   |||| | |  |  | ||   ||   |  |   | ||   ||
Db       4580 AAAATATTCAAAATTAAACCTATAATCAATCAAAATAAAATAAAATCTATTTCTTAATTT 4521

Qy       1127 AGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCT 1186
              | | ||      | || |     || |  | |  ||  ||   || |||   |  |||||
Db       4520 ATTTATTTATTTATTTTTTTTTTATTTTATTTATTTATTTATTTTTTTAAAATAAAATCT 4461

Qy       1187 GAGAAAACAGTCTTAACAAAAAAAAAAAAAAA 1218
                 |  | |  ||| |||| | || || |
Db       4460 CGCCCTATCGCCCAAACTAAAATACAATAACA 4429


RESULT 12
US-10-312-841-1/c
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
;  APPLICANT: Epigenomics AG
;  TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
;  FILE REFERENCE: E01/1208/WO
;  CURRENT APPLICATION NUMBER: US/10/312,841
;  CURRENT FILING DATE:  2002-12-30
;  NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
;   LENGTH: 3673778
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (3294164)
US-10-312-841-1

  Query Match             4.2%;  Score 51.2;  DB 15;  Length 3673778;
  Best Local Similarity   47.0%;  Pred. No. 34;
  Matches  190;  Conservative    0;  Mismatches  213;  Indels    1;  Gaps    1;

Qy        815 TATTCTTGTTGGAAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATT 874
              | ||| | ||  || | |  ||||  ||   | | ||   |  | |  || |||   |||
Db    1656921 TTTTCATATTCAAATTTAAAAAAAAAAACCTATAATCACTAACATATCCAATTTCTAATT 1656862

Qy        875 TTTCGAACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACT 934
              |||| || |  | |    | |  | ||   ||  |||  |  | |   | | |  | |
Db    1656861 TTTCAAATAAAATTTCTTATCTACAACAATAAACATTTTAAATAAAACTATTTTTAAAAT 1656802

Qy        935 TATTATGGGTGGTATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTA 994
              ||         |  | | |||    |  || |   ||  |  | |  || |||   | || |
Db    1656801 TAAATACATTTATTTTTAAATAAAACCTAATTTTCTATAATCCATATCAATAATTCTCAA 1656742

Qy        995 CAGATTACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGAT 1054
                || ||  ||   |    | |||   |   | ||| ||| |  |         || ||
Db    1656741 ACTCTTTCCATAAAAAC-ACACTTAAAAACGACAAAATAAAACATTTTTCTTAAAAACAT 1656683

Qy       1055 TCATGAAGGACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAAT 1114
                |   |   |  |  | ||||   | ||    ||  |||| |  || | ||| | |
Db    1656682 AAACTTAATCTCATTAACTCAAAACAAACTCCAAATAACTTAAAAATTTTAAATTTTATT 1656623

Qy       1115 GCATATTTTATTAGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATT 1174
                |||| ||| |  |||| || |  |  || ||   | |        | || |  || |
Db    1656622 TTATATATTAATTTTAATTTTACCTTTAATATCAATCATCTATATAAATTTTAAAATAAT 1656563

Qy       1175 ACTTTTTAATCTGAGAAAACAGTCTTAACAAAAAAAAAAAAAAA 1218
                || ||||   | ||||  |      |  | ||  ||| |||||
Db    1656562 TTCTTCTAATTCTATAAAAAATATCAATAATAATTAAATAAAAA 1656519


RESULT 13
US-10-311-455-1900
; Sequence 1900, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
;  TITLE OF INVENTION:  cytosine methylation
;  FILE REFERENCE: 5013.1014
;  CURRENT APPLICATION NUMBER: US/10/311,455
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: PCT/EP01/07537
;  PRIOR FILING DATE: 2001-07-02
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1900
;   LENGTH: 13427
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
```

```
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1900

  Query Match             4.1%;  Score 50.4;  DB 15;  Length 13427;
  Best Local Similarity   45.3%;  Pred. No. 4.7;
  Matches  223;  Conservative    0;  Mismatches  266;  Indels    3;  Gaps    1;

Qy        707 TTATGAATTTGAAGGAATCTTCCTTGCCTTGCACTGGGTATTATTATTCAACTAAAACTT 766
              || | ||||| || | |   | ||          |  |||| ||  |     |  | ||
Db       3718 TTGTTAATTTTAATGTAGATAATTAGTAGGTTGATTTTTATTTTTTATTTTATTTTATTT 3777

Qy        767 CTATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTGG 826
               ||  |  ||  | |||     || |    | |     ||   ||   || ||  | ||
Db       3778 TTAAGTATTATATATTTTATTTTTTAAGTATTATAGTAGAAGGAGTTTATTTTTTAGTTG 3837

Qy        827 AAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCA 886
              |||| ||| |  |  |   | |   ||  |    |   |||    ||||     |
Db       3838 AAATTATGTATGTTGATGTGAGTATAAATAATTTGTGGTATTAGAGATTTTAATTAAAAT 3897

Qy        887 AATAGCTGCAAGCAGAAACTACGCTTT---CCACGACATATTCTCTCTACTTATTATGGG 943
              | |    |  ||  | | | ||   |||      | |  ||||| | | ||  |  |||
Db       3898 ATTTTTTTTAAAGAAATATTATAATTTTTAATAAGTTATATTATTTTTATATGATATATA 3957

Qy        944 TGGTATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACC 1003
              || | |||||  ||| |  ||  | | ||  |   ||| |      || || |  ||
Db       3958 TGTTTTGTAAGTTTATATAAAATTTAAATTGGTTAAATAGAAAATGTTGTAAAATTTTTG 4017

Qy       1004 CAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGG 1063
              ||||  |  |    |||||        | || ||    ||||   | || ||      || |
Db       4018 AAAAGTTATTTGTTTAATTTTATTGAATTTTAATTTTTGGATTGTAAAAATAAGATAATG 4077

Qy       1064 ACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTT 1123
              |    |  || | |    |  | || |   || ||||| |  | |   |    ||||||
Db       4078 ATAGTTAATTTATAGGGTTTTATTATGGATGAAATTAAATATTGTATGTAAAAGTATTTT 4137

Qy       1124 ATTAGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAA 1183
              | | | | |  || | || |   ||||||    |  |    ||    |||  || | ||
Db       4138 GTAAATGAAAAAAAAATTTTTTTTAAATGTAGATTATTAATATTTTAAATTTTTTATAAA 4197

Qy       1184 TCTGAGAAAACA 1195
                | |  | | |
Db       4198 GTTTAATATAGA 4209


RESULT 14
US-10-311-455-768/c
; Sequence 768, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
;  TITLE OF INVENTION:  cytosine methylation
;  FILE REFERENCE: 5013.1014
;  CURRENT APPLICATION NUMBER: US/10/311,455
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: PCT/EP01/07537
;  PRIOR FILING DATE: 2001-07-02
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 768
;   LENGTH: 8951
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-768

  Query Match             4.1%;  Score 50;  DB 15;  Length 8951;
  Best Local Similarity   44.1%;  Pred. No. 4.8;
  Matches  209;  Conservative    0;  Mismatches  265;  Indels    0;  Gaps    0;

Qy        746 ATTATTATTCAACTAAAACTTCTATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTT 805
              ||||  |   || || ||  |    ||| |   |||  || |||  |    | ||| |
Db       1019 ATTACAAAAAAAATACAAAATAACAATCCTCCCTCTAACTTAATAAAAATATATTTTTTC 960

Qy        806 CAGTGCTTCTATTCTTGTTGGAAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCAC 865
              ||       |||   | ||    |  || ||||  || | ||| |  |||  |   || |
Db        959 CATAAAACATATATATATTTTTACAAATAAAAAAATAATTTAAAATAAAAACATATATTTC 900

Qy        866 TTTACCATTTTTCGAACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATT 925
              |  |  |  |  || |  |  ||    |  || |  | |  ||| |||  |   |||
Db        899 TACTCTTTAAATTAAAAAAAACTTAAAATCTTTCAAATTCAATACTTCCCAAAAATAATT 840

Qy        926 CTCTCTACTTATTATGGGTGGTATGTAATATTAGACTGAACATCACTTTTTCCCATAAAT 985
              || |     | |    |  |   ||   |     | |  || | |||| |   | |
Db        839 TTCCTTTTAATTAAAATTTTATTCTTATATTACTTTTTACTATTATTTTTACAATTTACC 780

Qy        986 TCCTTTCTACAGATTACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAA 1045
              |  |    | | | |  | ||| ||    | |  |||     | ||||     |   |
Db        779 TAATACTAATAAAATCTCAAAAACTATATTTAATATTAAAATATAATTTTTCCAAAAAAT 720

Qy       1046 CCTTAAGATTCATGAAGGACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTT 1105
                || | | |  ||   ||  ||||    ||         ||  |    ||| ||||||
Db        719 AACAAATAATTAATAATCTCCCCTTTTCCTCAACAACATAATTATACCCAAAAAAAATTT 660

Qy       1106 ATTTTAAATGCATATTTTATTAGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGT 1165
              || || ||   |  |  |||  || |  || ||   ||   ||      ||  | |
Db        659 ATCTTTAAAAAAATATAATTTATAAAAAAAAAAAAAAAATAAATAAATAAATAAAATATAA 600

Qy       1166 TTACTTATTACTTTTTAATCTGAGAAAACAGTCTTAACAAAAAAAAAAAAAAAA 1219
              |   | |||   | |||  |   || |      ||  ||||||   | | ||
Db        599 TACAATTTTAAAAATAAATTTTTAAATAACCCAAAAAATAAAAAACCTACACAA 546


RESULT 15
US-10-311-455-860
; Sequence 860, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
;  TITLE OF INVENTION:  cytosine methylation
;  FILE REFERENCE: 5013.1014
;  CURRENT APPLICATION NUMBER: US/10/311,455
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: PCT/EP01/07537
;  PRIOR FILING DATE: 2001-07-02
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 860
;   LENGTH: 16439
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-860

  Query Match             4.1%;  Score 50;  DB 15;  Length 16439;
  Best Local Similarity   50.0%;  Pred. No. 6.3;
  Matches  155;  Conservative    0;  Mismatches  150;  Indels    5;  Gaps    1;

Qy        912 TTCCACGACATATTCTCTCTACTTATTATGGGTGGTATGTAATATTAGACTGAACATCAC 971
              ||  |  | || || |   || || || |  ||  |  | ||||||    | ||  |
Db       5272 TTATAAAAAATTTTTTAGGTAGTTTTTTTTTGTTTTTAGGAATATTTATGTTAATTTATT 5331
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Qy        972 TTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAGCTCGT-----GTCATAATTGCTG 1026
              ||||    | | |||     | |  |||| |     | | | ||       | | ||||  |
Db       5332 ATTTTTAGAGATATTAGAATATGAAGATAAGAGTATGATAGTTTTCGTTTAAAATTTTTT 5391

Qy       1027 AAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTTTGAAAAATCTCACC 1086
              ||   | |  | |  | ||  |     |       |||  | |  ||  ||    | |
Db       5392 AATGGTAATTGGAAGGAAAGGTATTTTTGGGGTTTGGATTTTTAATTTTAATTGGTTAAT 5451

Qy       1087 TTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTAGTAATACTAACAATTGTAG 1146
              ||| ||||| | ||| ||| |||||     ||||||| ||   || | | | || | |
Db       5452 TTTTAAAATTATTAAGTTTTTTTTATTATTATATTTTTTTTTAAAGATTGAAAAATATTT 5511

Qy       1147 GAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAAACAGTCTTAACAAA 1206
                |||   || |   || ||| |  |    |||  ||  |  | | |        || |||
Db       5512 ATAATTATTTTTTTGTTATTTTCGGAAATGTTTGGAAGGTAGGTAGAGTTAAAAAAAAAA 5571

Qy       1207 AAAAAAAAAA 1216
              ||||||||||
Db       5572 AAAAAAAAAA 5581
```

Search completed: January 19, 2005, 17:17:33
Job time : 772 secs

GenCore version 5.1.6


OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 12:54:40 ; Search time 371 Seconds
(without alignments)
2335.449 Million cell updates/sec

Title: US-10-070-666A-1
Perfect score: 1219
Sequence: 1 agtaagcaaactaaatttaa.....taacaaaaaaaaaaaaaaaa 1219

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| | 1 | 58.4 | 4.8 | 1141 | 4 | US-09-806-708B-22 | Sequence 22, Appl |
| c | 2 | 54.4 | 4.5 | 1141 | 4 | US-09-806-708B-22 | Sequence 22, Appl |
| | 3 | 52 | 4.3 | 640681 | 4 | US-09-790-988-1 | Sequence 1, Appli |
| | 4 | 47.8 | 3.9 | 832 | 4 | US-09-621-976-2813 | Sequence 2813, Ap |
| c | 5 | 45.6 | 3.7 | 640681 | 4 | US-09-790-988-1 | Sequence 1, Appli |
| | 6 | 45.4 | 3.7 | 1436 | 4 | US-09-614-912-35 | Sequence 35, Appl |
| | 7 | 44 | 3.6 | 11049 | 4 | US-10-204-708-22 | Sequence 22, Appl |
| | 8 | 43.8 | 3.6 | 2949 | 3 | US-09-412-554A-3 | Sequence 3, Appli |
| c | 9 | 43.8 | 3.6 | 51952 | 3 | US-08-947-823-1 | Sequence 1, Appli |
| c | 10 | 43.4 | 3.6 | 826 | 4 | US-09-270-767-29614 | Sequence 29614, A |
| c | 11 | 43.4 | 3.6 | 1348 | 4 | US-09-270-767-13608 | Sequence 13608, A |
| c | 12 | 43.4 | 3.6 | 2999 | 4 | US-09-710-279-3580 | Sequence 3580, Ap |
| c | 13 | 43.4 | 3.6 | 3099 | 4 | US-09-710-279-4201 | Sequence 4201, Ap |
| | 14 | 43.4 | 3.6 | 3501 | 4 | US-09-710-279-3614 | Sequence 3614, Ap |
| c | 15 | 43.4 | 3.6 | 4015 | 4 | US-09-710-279-3619 | Sequence 3619, Ap |
| | 16 | 43.4 | 3.6 | 4207 | 4 | US-09-710-279-3631 | Sequence 3631, Ap |
| | 17 | 43.2 | 3.5 | 2141 | 4 | US-09-270-767-25196 | Sequence 25196, A |
| | 18 | 43.2 | 3.5 | 3016 | 4 | US-09-270-767-9898 | Sequence 9898, Ap |
| c | 19 | 43 | 3.5 | 1422 | 1 | US-08-319-704-5 | Sequence 5, Appli |
| | 20 | 42.4 | 3.5 | 10640 | 4 | US-09-417-485D-5 | Sequence 5, Appli |
| c | 21 | 41.4 | 3.4 | 665 | 3 | US-08-998-416-937 | Sequence 937, App |
| | 22 | 41.4 | 3.4 | 3618 | 1 | US-07-872-678A-36 | Sequence 36, Appl |
| | 23 | 41.2 | 3.4 | 6801 | 4 | US-10-204-708-62 | Sequence 62, Appl |
| | 24 | ~ 41 | 3.4 | 5852 | 1 | US-07-867-106-2 | Sequence 2, Appli |
| | 25 | 40.8 | 3.3 | 526 | 4 | US-08-956-171E-516 | Sequence 516, App |
| | 26 | 40.8 | 3.3 | 526 | 4 | US-08-781-986A-516 | Sequence 516, App |
| | 27 | 40.8 | 3.3 | 1055 | 4 | US-09-806-708B-23 | Sequence 23, Appl |
| | 28 | 40.8 | 3.3 | 1905 | 4 | US-09-270-767-10264 | Sequence 10264, A |
| c | 29 | 40.8 | 3.3 | 20674 | 4 | US-09-641-638-651 | Sequence 651, App |
| c | 30 | 40.8 | 3.3 | 20674 | 4 | US-10-170-097-651 | Sequence 651, App |
| c | 31 | 40.6 | 3.3 | 58407 | 4 | US-08-916-421B-2 | Sequence 2, Appli |
| c | 32 | 40.6 | 3.3 | 58407 | 4 | US-09-692-570-2 | Sequence 2, Appli |
| c | 33 | 40.4 | 3.3 | 19124 | 2 | US-08-487-826B-13 | Sequence 13, Appl |
| c | 34 | 40.2 | 3.3 | 837 | 3 | US-08-998-416-288 | Sequence 288, App |
| c | 35 | 40 | 3.3 | 665 | 2 | US-08-883-795A-36 | Sequence 36, Appl |
| c | 36 | 40 | 3.3 | 832 | 4 | US-09-621-976-2813 | Sequence 2813, Ap |
| c | 37 | 40 | 3.3 | 1055 | 4 | US-09-806-708B-23 | Sequence 23, Appl |
| | 38 | 40 | 3.3 | 2058 | 2 | US-08-749-391-1 | Sequence 1, Appli |
| | 39 | 40 | 3.3 | 2058 | 3 | US-09-390-200-1 | Sequence 1, Appli |
| c | 40 | 40 | 3.3 | 162450 | 3 | US-09-345-882-1 | Sequence 1, Appli |
| c | 41 | 39.8 | 3.3 | 319608 | 4 | US-09-539-333D-1 | Sequence 1, Appli |
| c | 42 | 39.8 | 3.3 | 319608 | 4 | US-09-679-409-1 | Sequence 1, Appli |
| c | 43 | 39.6 | 3.2 | 355 | 4 | US-09-621-976-15488 | Sequence 15488, A |
| | 44 | 39.6 | 3.2 | 6583 | 4 | US-10-204-708-25 | Sequence 25, Appl |
| | 45 | 39.6 | 3.2 | 11131 | 4 | US-10-204-708-27 | Sequence 27, Appl |

ALIGNMENTS

RESULT 1
US-09-806-708B-22
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
US-09-806-708B-22

Query Match 4.8%; Score 58.4; DB 4; Length 1141;
Best Local Similarity 11.9%; Pred. No. 0.00022;
Matches 83; Conservative 261; Mismatches 352; Indels 4; Gaps 1;

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Qy      518 AAAATTCGCTTTAGTCTACGCTCCTCTTTGTGGTGGTTTCTCTAATAAATGGTGGGGTAG 577
            :::| :  :::: :|       | : : ::::::|: :::    |  :::: ::      |
Db      129 RWRAMBDTVDHHYVTAMNNAWTTMCMMDKDDKRTRWWWKKNNNATGWDDDTKYHMWNNNG 188

Qy      578 GAAGCACAATCAACATCATATGTTCACAAACAACATTCTAAAGGACGAAGATATCTAACA 637
              : :::::  : ::: ::  : :  :       :|:::::::::|:: :: :  |:  :
Db      189 CBTVTWMVRYKTDRDWSBKRMNYGMBWWKNWSYDVTYYWWVWDDMCKRKVRRWVRTRGRM 248

Qy      638 CGATTACAAATTGTGGTAATTCCCCTTCTTATTTTTAAAGTGGAAATTAGACTCCATCTT 697
                |   |: :     :|: : :   |       | |  ::|  : : : ::  ||||
Db      249 RNYMVAWBTAHRRRYNNGWTBAMAYRRWTMNNNNNNAKAMCKRAKYWGWNRABVNSTCTT 308

Qy      698 AGCTTCTTATTATGAATTTGAAGGAATCTTCCTTGCCTTGCACTGGGTATTATTATTCAA 757
            ::::| : :|  :       |:| :::: :: :    :::        | ::| :    ::
Db      309 WKSKTTKVRTSCWANNCRAGDANKDHKWWKWSAAMGVYWNNNNNNNWTYKKARHBARWDW 368

Qy      758 CTAAAACTTCTATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTAT 817
            ::: |: :::   |:::   :|::: | :    ||  :: : ::::::: : : |:
Db      369 VWHSAWKKWHANAAHYSRKKWTBYKRKTMVNNNGTTMWKRMWAWYWKMDMDWBGTYNNN 428

Qy      818 TCTTGTTGGAAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTT 877
              :|: |:           ::|   :::|::::        :: : |::  | ::  |
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Db        429 NNGGRTYYGWTKNKKMWTYYKWKANNCKWRAWDHKTCTHNNTTWWKMKTYWNNCYWKSMT 488

Qy        878 CGAACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTAT 937

Db        489 NGKSHRBAAAVYTWYMWWWRRYAHANNNNWDYWWKACTWYKYBVCSKWWNNYAAWYTKSS 548

Qy        938 TATGGGTGGTATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAG 997

Db        549 WNYTSRYYRWKTNNSWRWRSDTRSMGRANNYARABHYGYKWNTRWWBWSHTWBHBRAGAA 608

Qy        998 ATTACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCA 1057

Db        609 HYWMBMMYBAKCHCMKAWY----KAKKYAGAGGSNNNNNNNNNNNNNNNNATCARDDYYA 664

Qy       1058 TGAAGGACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCA 1117

Db        665 ASRWYAMANAKWYYYKBAANNAYYTHANNWWGCWNNATDTRRTMWKNNNNNNAGTWKNNN 724

Qy       1118 TATTTTATTAGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACT 1177

Db        725 NNNAKNASAAKNYAAAAVKAAKKHWRWANKWAMRGWHADAAABTTDKRNNGAYTKYTTTN 784

Qy       1178 TTTTAATCTGAGAAAACAGTCTTAACAAAAAAAAAAAAAA 1217

Db        785 NNNTYRGVVTNTAARDGWANNNNNNNNNNNNNGWSDMWV 824


RESULT 2
US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
;  APPLICANT: The University of British Columbia
;  TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
;  FILE REFERENCE: 4810-58741
;  CURRENT APPLICATION NUMBER: US/09/806,708B
;  CURRENT FILING DATE:  2001-04-03
;  PRIOR APPLICATION NUMBER: US 60/147,133
;  PRIOR FILING DATE: 1999-08-04
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
;   LENGTH: 1141
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (1)..(1141)
;   OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
US-09-806-708B-22

  Query Match             4.5%;  Score 54.4;  DB 4;  Length 1141;
  Best Local Similarity   11.8%;  Pred. No. 0.0018;
  Matches  127;  Conservative  374;  Mismatches  566;  Indels   11;  Gaps    2;

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Db        1124 TYKKANNNNNNNNGMGKDWNRMDATKWSATGTAWWTNHAKRGATMCWYWYWTGTNRRWCM 1065

Qy          76 AACCCGAACTTCTCAACGAATACAAATTTATTTACAAGGATACTGAATATGACTGCACTG 135

Db        1064 RTYAMRTWYTRSNANWSCATKBMWWTMKWYATKYRTAWYAMWCAWRNNNMWCATNGYAKS 1005

Qy         136 AATATGCTAAATCAAATAAGCATCCTGGCGGTCTTAATTTCCTCAATTTGTTTATTGATG 195

Db        1004 CATNNAMWYATTRWAAYAAAKWARWAGNNMRMYGAAAGNKWGCMAAMATMGBWWADTAGK 945

Qy         196 AGAAGTAAGATTTGACTGAATATTTCAGAACACTCCATTCTAAGTAGGCTTTGAAAATTT 255

Db         944 MCNNNNNNWTTDVRRMAMKAKNNNNNNAYWTACYNRAATNNKMATHWMKWTHGAHSKRRT 885

Qy         256 TAAAATCCTTCCCTAAGACTGGCGCAAAATAAGAGGAGACTGAATCTTCAAAGAGATTCT 315

Db         884 RHHTRTCRRTKYNNNNNNARTVYWYHHAARRWMNAWWTRTNNNNNNNNNNACRNTRTWWA 825

Qy         316 CAATATTAAAGAAAAAGCTTAAGCATTTATTCGAACCAAACTGGCCTATCGAAATTGGTT 375

Db         824 BWKHSWCNNNNNNNNNNNNNNTWCHYTTANABBCYRANNNNAAARMARTCNNYMHAAVTT 765

Qy         376 TATTCTTAACTACCTTTACTTTATTTGTCACTGGATGTTTGACTCAAAAGTGGTATTTCT 435

Db         764 THTDWCYKTWMNTWYWDMMTTMBTTTTRNMTTSTNMTNNNNNNMWACTNNNNNNMWKAYY 705

Qy         436 CTATTCCCCTTCTTGTCTTAATGCAAATCATCAGTGGTTGGATTGGTCACTCTATGAACC 495

Db         704 AHATNNWGCWWNNTDARRTNNTTVMRRRWMTNTKTRWYSTTRRHHYTGATNNNNNNNNNN 645

Qy         496 ACAATCGTAACCCTATATTAAGAAAATTCGCTTTAGTCTACGCTCCTCTTTGTGGTGGTT 555

Db         644 NNNNNNSCCTCTRMMTMRWTMKGDGMTVRKKVKWRDTTCTYVDVWADSWVWWYANWMRCR 585

Qy         556 TCTCTAATAAATGGTGGGGTAGGAAGCACAATCAACATCATATGTTCACAAACAACATTC 615

Db         584 DVTYTRNNTYCKSYAHSYWYWSNNAMWYRRYSARNWSSMARWTTRNNWWMSGBVRMRWAG 525

Qy         616 TAAAGGACGAAGATATCTAACACGATTACAAATTGTGGTAATTCCCCTTCTTATTTTTAA 675

Db         524 TMWWRHWNNNNTDTRYYWWWKRWARBT-----TTVYDSMCNAKSMWRGNNWRAMKMWWAA 470

Qy         676 AGTGGAAATTAGACTCCATCTTAGCTTCTTATTATGAATTTGAAGGAATCTTCCTTGCCT 735

Db         469 NNDAGAMDHWTYWMGNNTMWMRRAWKMMNMAWCRRAYCCNNNNNRACVWHKHKMWRWTWK 410

Qy         736 TGCACTGGGTATTATTATTCAACTAAAACTTCTATATCGTAATTCTTTCTGAATTGATTG 795

Db         409 YMWKAACNNNNBKAMYMRVAWMMYSRDTTNTDWMMWTSDWBWHWYTVDYTMMRAWNNNNN 350

Qy         796 CTGGTTTCTTCAGTGCTTCTATTCTTGTTGGAAATCATGAAAATGAAATGAAATTCGAAA 855

Db         349 NNWRBCKTTSWMWWMDHMNTHCTYGNNTWGSAYB------MAAMSMWAAGASNBVTYNWC 296

Qy         856 GAAGAATCACTTTACCATTTTTCGAACATCAAATAGCTGCAAGCAGAAACTACGCTTTCC 915

Db         295 WRMTYMGKTMTNNNNNNKAWYYRTKTVAWCNNRYYYDTAVWTBKRNYKYCYAYBWYYBMY 236

Qy         916 ACGACATATTCTCTCTACTTATTATGGGTGGTATGTAATATTAGACTGAACATCACTTTT 975

Db         235 MGKHHWBWWRRABHRSWNMWWVKCRNKYMVSWHYHAMRYBKWABAVGCNNNWKDRMAHHH 176

Qy         976 TCCCATAAATTCCTTTCTACAGATTACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAA 1035

Db         175 WCATNNNMMWWWYAYMHHMHKKGKAAWTNNKTABRDDHBAHVKTYWYWRYDYWCAMCWMN 116

Qy        1036 AGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTTTGAAAAATCTCACCTTTGAAA 1093

Db         115 AKAKVRTAMKHMWYYTDRYVSANNTGVRWMMMRWCMWWYSMNNRWYYRMGRKYTWAWM 58


RESULT 3
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
;  APPLICANT: SHIGENOBU, SHUJI
;  APPLICANT:  WATANABE, HIDEMI
;  APPLICANT:  HATTORI, MASAHIRA
;  APPLICANT:  SAKAKI, YOSHIYUKI
;  TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
;  FILE REFERENCE: 081356/0159
;  CURRENT APPLICATION NUMBER: US/09/790,988
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: JP2000-107160
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
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;   LENGTH: 640681
;   TYPE: DNA
;   ORGANISM: Buchnera sp.
US-09-790-988-1

  Query Match             4.3%;  Score 52;  DB 4;  Length 640681;
  Best Local Similarity   54.8%;  Pred. No. 0.04;
  Matches  103;  Conservative    0;  Mismatches   85;  Indels    0;  Gaps    0;

Qy       1031 ATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTTTGAAAAATCTCACCTTTG 1090
              | |||| || |   |   ||  ||  || |  ||  ||||||| ||||||||      |
Db      95585 AGTAAAAAAATATTAATATACTATCAATAATTGAAATATTTTTTAAAAATCTTTTTCTAT 95644

Qy       1091 AAAATAAATAAATTTATTTTAAATGCATATTTTATTAGTAATACTAACAATTGTAGGAAA 1150
              || ||| | |||| || || ||      |  ||||  | | |  ||  ||| ||  |
Db      95645 TTAAAAAACATATTTTTTATATATCTGACTAGTATTTTTTAAAAAAATCATTTTAATATT 95704

Qy       1151 TGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAAACAGTCTTAACAAAAAAA 1210
              | | | ||  |    | | || ||| | || |      |  |  |||| |  | |||| ||
Db      95705 TTTTTGATATTAAAATGATTTTTTATTCTTAATATATATTATTCAGTTTATATAAAATAA 95764

Qy       1211 AAAAAAAA 1218
              ||||  | |
Db      95765 AAAATATA 95772


RESULT 4
US-09-621-976-2813
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 2813
;   LENGTH: 832
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 235..399
US-09-621-976-2813

  Query Match             3.9%;  Score 47.8;  DB 4;  Length 832;
  Best Local Similarity   17.4%;  Pred. No. 0.054;
  Matches   78;  Conservative  169;  Mismatches  201;  Indels    1;  Gaps    1;

Qy        692 CATCTTAGCTTCTTATTATGAATTTGAAGGAATCTTCCTTGCCTTGCACTGGGTATTATT 751
              ::::::   |:: : :| ::: : : :  :: :::|:  ::  ::: : :  :|:|::::
Db          1 YRWYWWKYTTWYAKCWTKWKWSWSYWMYWKWYYMKTYWRWRRKKKKAWWKYWKTWTWWYW 60

Qy        752 ATTCAACTAAAACTTCTATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTTCAGTGC 811
              :: ::  :   |:   : : : ::   ::::: ::: :  ::|: : |: ::  :: :
Db         61 RYAMWGTYKKKAMCRTKTKKKKKKGYMWMWYWGWRRSYMAMWTRTWTGYAYYRSMMYWWR 120

Qy        812 TTCTATTCTTGTTGGAAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACC 871
              : |: :: ::::|     : :| : :::;|: | :: :|: :|| :  :: |: : :: :
Db        121 YRCWKKKAYYRKTTCYSSKGWTWWKRWKKAWTTWWWKKTYYWAATRYWWMMCWTKRWRAS 180

Qy        872 ATTTTTCGAACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCT 931
              ::: :: | |  :: ::: ::: :|::  :   :   |   : :: :: ::: : |
Db        181 WWYCWWWGKARKWSTWRKSRSYASARSAKRCCYSCSWGAMSWKYMWRMWRWRGWATGAGM 240

Qy        932 ACTTATTATGGGTGGTATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTT 991
              : |  : :::: |: :     ::          | | | :| ::|:     :: :   ::
Db        241 KAWRASCMMRRKYAGKSKTSYKSMWMCWTRSWKYCYTKARWTGYYCYRKGGMWGKRGRWY 300
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Qy        992 CTACAGATTACCCAAAGCTCGTGTCATAATTG-CTGAAGAATTAAAGAAGTGGAACCTTA 1050
              :: :  |:|: : ::||| | ::: : :: ::  ::: |: :| :: :|: : :
Db        301 ASKKYMWKRWWWCWARMYRYSTGTRASMWWRRWYYTMMMKWWKYAWARAAWRWWAMWWAW 360

Qy       1051 AGATTCATGAAGGACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTT 1110
              ::|   |  |      | | |   | || |||     || |  | |  |  | ||| ||
Db        361 RRACAAAATATAATTATTTATGGTACAATTCTTGTACTTTAGCAAATCTGGAGTTAGTTC 420

Qy       1111 AAATGCATATTTTATTAGTAATACTAACA 1139
              | |  || | |   ||| || | || | |
Db        421 ATAGTCAAAGTCAGTTAATATTTCTTAGA 449


RESULT 5
US-09-790-988-1/c
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
;  APPLICANT: SHIGENOBU, SHUJI
;  APPLICANT:  WATANABE, HIDEMI
;  APPLICANT:  HATTORI, MASAHIRA
;  APPLICANT:  SAKAKI, YOSHIYUKI
;  TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
;  FILE REFERENCE: 081356/0159
;  CURRENT APPLICATION NUMBER: US/09/790,988
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: JP2000-107160
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 640681
;   TYPE: DNA
;   ORGANISM: Buchnera sp.
US-09-790-988-1

  Query Match             3.7%;  Score 45.6;  DB 4;  Length 640681;
  Best Local Similarity   44.6%;  Pred. No. 1.2;
  Matches  267;  Conservative    0;  Mismatches  324;  Indels    7;  Gaps    2;

Qy        622 ACGAAGATATCTAACACGATTACAAATTGTGGTAATTCCCCTTCTTATTTTTAAAGTGGA 681
              | | | | || |||  | |||| |||||  |  || ||    |  |  |||| | | |
Db     455530 AGGGATAAATATAATGCAATTAAAAATTTTTTTATTTAAATTATTATTTTTAATATTTTT 455471

Qy        682 AATTAGACTCCATCTTAGCTTCTTATTATGAATTTGAAGGAATCTTCCTTGCCTTGCACT 741
                    |  ||  ||  |||  || |||        |||  ||  |    | |
Db     455470 TTCGTTTTCTTTTAATAATTTTGCATTCGGATTTTTTTTTAATAATCGATATGATTCTAA 455411

Qy        742 GGGTATTATTATTCAACTAAAACTTCTATATCGTAATTCTTTCTGAATTGATTGCTGGTT 801
              | |||||  | ||  | |       | ||  || || |||    ||   ||  || ||
Db     455410 TTTTTTTATTGATAAAAAATATACAAAAGATTTTATTTTTTTTAAAAAAAATGAATGTTT 455351

Qy        802 TCTTCAGTGCTTCTATTCTTGTTGGAAATCATGAAAATGAAATGAAATTCGAAAGAAGAA 861
              |  |   |     |||            |  | |||   |||     |||       || ||
Db     455350 TTCTTTTTTAAAATATAAAAAAAATTTTTTTTTAAATAAAAAAATTATTATTGGCAATAA 455291

Qy        862 TCACTTTACCATTTTTCGAACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACA 921
              |||  ||||    ||||      |  ||||||  |  ||| | |   ||   | |  |   |
Db     455290 TCATTTTATTGGTTTTTTTCAAAAAAATAGATTTAAG-ATATTTTATATTGTGAAATCAA 455232

Qy        922 TATTCTCTCTACTTATTATGGGTGGTATGTAATATTAGACTGAACATCACTTTTTCCCAT 981
              |  | |  |   |  ||| | |    |  |   ||| | | | | ||| | || |    ||
Db     455231 AAGACACGATGTATTCTATTGCTAAAAATTCTGGTTATAATTATCATGAATTATCTAAAT 455172

Qy        982 AAATTCCTTTCTACAGATTACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGT 1041
              |  :|| || | | |       |||       | || || | | || || ||  || |
Db     455171 TTAACTCTATCAAAAAACCTTATAAA------ATAATTATAGGTCAAAAAATATGGATGG 455118

Qy       1042 GGAACCTTAAGATTCATGAAGGACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAA 1101
              |  |  ||  ||| || ||     || |  |     ||    || | || |||  |
Db     455117 GAGATTTTTTAATTGATAAAAATAATAATGATTGTTCTATTCTAAATTTAGAAAAAAACA 455058

Qy       1102 ATTTATTTTAAATGCATATTTTATTAGTAATACTAACAATTGTAGGAAATGTGTTATGGT 1161
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Db     455057 GTATAAAACAACATAATTCTTGTGAAGTTGTTTTTAAAAATTTATTAAATATTGAAAAAT 454998

Qy       1162 TTGTTTACTTATTACTTTTTAATCTGAGAAAACAGTCTTAACAAAAAAAAAAAAAAAAA 1219

Db     454997 TTTTGAAAGATAATATAAAAACTAAAAAAATATGTTTTTTTTGCATAAAAAAAATAAA 454940
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RESULT 6
US-09-614-912-35
; Sequence 35, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Caimi, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 35
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Zea mays
US-09-614-912-35

Query Match 3.7%; Score 45.4; DB 4; Length 1436;
Best Local Similarity 65.0%; Pred. No. 0.22;
Matches 67; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

```
Qy       1117 ATATTTTATTAGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTAC 1176

Db       1330 ATAGTATAATAATAATAATAAAATAGCAAGTAATAGTTGTATCGTATTATTATTAATTAA 1389

Qy       1177 TTTTTAATCTGAGAAAACAGTCTTAACAAAAAAAAAAAAAAAA 1219

Db       1390 TTTATTAGCTGGTAGGCAAGTAGTATTAAAAAAAAAAAAAAA 1432
```

RESULT 7
US-10-204-708-22
; Sequence 22, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 22
; LENGTH: 11049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-22

Query Match 3.6%; Score 44; DB 4; Length 11049;
Best Local Similarity 44.7%; Pred. No. 0.85;
Matches 170; Conservative 0; Mismatches 210; Indels 0; Gaps 0;

```
Qy         12 TAAATTTAAAAAACAAGCATTATGGGAGTTGATAAGACTTAAGAAGAAATTGTTCTTGAA 71

Db       3371 TAATTTGAAAATATTTGTATAATTTGATTTGTTTAATTTTAGTAAGTTTATATACGTAAA 3430

Qy         72 AATAAACCCGAACTTCTCAACGAATACAAATTTATTTACAAGGATACTGAATATGACTGC 131

Db       3431 ATTAAATTTTTGCGGATAGAAAAGTTAAAATTTGTAGTAAAGTTAAAAATTATTTTCGGT 3490

Qy        132 ACTGAATATGCTAAATCAAATAAGCATCCTGGCGGTCTTAATTTCCTCAATTTGTTTATT 191

Db       3491 ATAAGATTTAAAGATTAATAATATTTTAATATAAAAAATAAGTTTTTTTAGTTTTTTAGT 3550

Qy        192 GATGAGAAGTAAGATTTGACTGAATATTTCAGAACACTCCATTCTAAGTAGGCTTTGAAA 251

Db       3551 TAGGTGATTTAAAAATTTTTATTAGTATATATAGTTTAAAGAGATGGTAATATTTTGTTA 3610

Qy        252 ATTTTAAAATCCTTCCCTAAGACTGGCGCAAAATAAGAGGAGACTGAATCTTCAAAGAGA 311

Db       3611 ATATATTTAAACGTATATTATAAATATTAAAATTTATAAGAGATAAAAGTTTAATTTATT 3670

Qy        312 TTCTCAATATTAAAGAAAAAGCTTAAGCATTTATTCGAACCAAACTGGCCTATCGAAATT 371

Db       3671 TTTGTATTATTTGATATAGATATTTAGATTGTATAAATAAGATATTAAGTTATATAGATG 3730

Qy        372 GGTTTATTCTTAACTACCTT 391

Db       3731 GTTTAAAGATTAAATAATTT 3750
```

RESULT 8
US-09-412-554A-3
; Sequence 3, Application US/09412554A
; Patent No. 6355788
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell
; APPLICANT: Ellsworth, Jeff L.
; TITLE OF INVENTION: FOLLISTATIN RELATED PROTEIN ZFSTA2
; FILE REFERENCE: 98-50
; CURRENT APPLICATION NUMBER: US/09/412,554A
; CURRENT FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2949
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Degenerate oligonucleotide sequence encoding the
; OTHER INFORMATION: zfsta2 polypeptide of SEQ ID NO:2.
; NAME/KEY: variation

```
;   LOCATION: (1)...(2949)
;   OTHER INFORMATION: Each N is independently any nucleotide.
US-09-412-554A-3

  Query Match             3.6%;  Score 43.8;  DB 3;  Length 2949;
  Best Local Similarity   30.3%;  Pred. No. 0.64;
  Matches   82;  Conservative   51;  Mismatches  138;  Indels    0;  Gaps    0;

Qy         73 ATAAACCCGAACTTCTCAACGAATACAAATTTATTTACAAGGATACTGAATATGACTGCA 132
              |:||:|| |    :   :  ||     |:||:  : | ||  |:  :||:    |: |
Db        290 AYAARCCNGTNTGYGGNWSNGAYGGNGARTTYTAYGARAAYCAYTGYGARGTNCAYMGNG 349

Qy        133 CTGAATATGCTAAATCAAATAAGCATCCTGGCGGTCTTAATTTCCTCAATTTGTTTATTG 192
              | |  | :   ||:  : | ||:  : |   :|  | :||:     :  :|| ||:|  |
Db        350 CNGCNTGYYTNAARAARCARAARATHACNATHGTNCAYAAYGARGAYTGYTTYTTYAARG 409

Qy        193 ATGAGAAGTAAGATTTGACTGAATATTTCAGAACACTCCATTCTAAGTAGGCTTTGAAAA 252
                || ||:|  |    || ||:||::  | :|      |:       :  | ::|  |:|
Db        410 GNGAYAARTGYAARACNACNGARTAYWSNAARATGAARAAYATGYTNYTNGAYYTNCARA 469

Qy        253 TTTTAAAATCCTTCCCTAAGACTGGCGCAAAATAAGAGGAGACTGAATCTTCAAAGAGAT 312
               :  :||:| : |:    |:     :| :||     | |    :||   ::: :  | :
Db        470 AYCARAARTAYATHATGCARGARAAYGARAAYCCNAAYGGNGAYGAYATHWSNMGNAARA 529

Qy        313 TCTCAATATTAAAGAAAAAGCTTAAGCATTT 343
               :   |  |  |  |:|  | |:||: |:||
Db        530 ARYTNYTNGTNGAYCARATGTTYAARTAYTT 560


RESULT 9
US-08-947-823-1/c
; Sequence 1, Application US/08947823
; Patent No. 6114605
;  GENERAL INFORMATION:
;    APPLICANT:  Williamson, Valerie M.
;    APPLICANT:  Kaloshian, Isgouhi
;    APPLICANT:  Yaghoobi, Jafar
;    APPLICANT:  Bodeau, John
;    APPLICANT:  Milligan, Stephen
;    TITLE OF INVENTION:  Procedures and Materials for Conferring
;    TITLE OF INVENTION:  Pest Resistance in Plants
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/947,823
;      FILING DATE:  09-OCT-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US97/18802
;      FILING DATE:  09-OCT-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/028,191
;      FILING DATE:  10-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bastian, Kevin L.
;      REGISTRATION NUMBER:  34,774
;      REFERENCE/DOCKET NUMBER:  02307O-070210US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  51952 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-947-823-1

  Query Match             3.6%;  Score 43.8;  DB 3;  Length 51952;
  Best Local Similarity   50.2%;  Pred. No. 1.5;
  Matches  108;  Conservative    0;  Mismatches  107;  Indels    0;  Gaps    0;

Qy        746 ATTATTATTCAACTAAAACTTCTATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTT 805
              ||||||||  |  || || || || ||  ||| | ||  |  |||   | |   ||
Db      12778 ATTATTATATACATATAAATTATAGATGATAAATATTAATAGATTAGATATTAAATTAGG 12719

Qy        806 CAGTGCTTCTATTCTTGTTGGAAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCAC 865
              | |  || ||        |  || |||| || ||  ||| |||||   |  |  ||  |
Db      12718 AATTAATTTTAGGAAGTCTAAAAGTCATTAACATTTAATTAAATTTATATAATCAAATAT 12659

Qy        866 TTTACCATTTTTCGAACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATT 925
              || |  |||||   |  ||  |||   |   |  || ||  |||   | ||      |
Db      12658 TTAAATATTTTATAACAATTTAATTTATAGTAAAAGTAAAAACGTAATTCAACTTTCAAC 12599

Qy        926 CTCTCTACTTATTATGGGTGGTATGTAATATTAGA 960
              | | || | ||| |    | ||| ||    || |
Db      12598 ATTTTTATTCATTCTTTTAGTTATATATATATATA 12564


RESULT 10
US-09-270-767-29614/c
; Sequence 29614, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29614
;   LENGTH: 826
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-09-270-767-29614

  Query Match             3.6%;  Score 43.4;  DB 4;  Length 826;
  Best Local Similarity   48.6%;  Pred. No. 0.55;
  Matches  119;  Conservative    0;  Mismatches  126;  Indels    0;  Gaps    0;

Qy        948 ATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAA 1007
              ||  |||| |  | | ||  |  |   |||  |  | |   ||| || | || || ||
Db        482 ATTAAATAGTTTATTCAATTTGTCAAGTTCTTAAGATTGTGTTTTTAGAAATGACACATC 423

Qy       1008 GCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCT 1067
                | | | |   |    |   |||  |||| || |   |  | |||||  |  |  ||
Db        422 TATTTTATAAACCTCTGCAAGTTATTCGAGAAATGCATTTTAGAAATTCAAAATCGGTCT 363

Qy       1068 ATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTA 1127
               ||||| |  ||   ||  | | ||| || |  | ||| ||   ||  |  | | ||| |
Db        362 TTTTTTTAGCAACAGCAATTCTTAAATTATACTACTTTTTTCCCAAATCGAAATATATAA 303

Qy       1128 GTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTG 1187
               |  |    | | |||||      || |  |   |  ||     ||||   |||  | ||
Db        302 CTTTTGTCTATATTTGTATATTGAGTATATTTCCTCTTTGTAAGATTAACATTTTGTTTG 243

Qy       1188 AGAAA 1192
                | |
Db        242 TTACA 238


RESULT 11
US-09-270-767-13608/c
```

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; Sequence 13608, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13608
;   LENGTH: 1348
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-09-270-767-13608

  Query Match             3.6%;  Score 43.4;  DB 4;  Length 1348;
  Best Local Similarity   48.6%;  Pred. No. 0.63;
  Matches  119;  Conservative    0;  Mismatches  126;  Indels    0;  Gaps    0;

Qy        948 ATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAA 1007
              ||  |||| |  | | ||  |  |   |||  |  | |   ||| || | || || ||
Db        482 ATTAAATAGTTTATTCAATTTGTCAAGTTCTTAAGATTGTGTTTTTAGAAATGACACATC 423

Qy       1008 GCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCT 1067
                | | | |   |     |   |||  |||| || |   |  | |||||  |  |  ||
Db        422 TATTTTATAAACCTCTGCAAGTTATTCGAGAAATGCATTTTAGAAATTCAAAATCGGTCT 363

Qy       1068 ATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTA 1127
              ||||| |  ||   ||  | | ||| || |  | ||| ||   ||  |  | | ||| |
Db        362 TTTTTTTAGCAACAGCAATTCTTAAATTATACTACTTTTTTCCCAAATCGAAATATATAA 303

Qy       1128 GTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTG 1187
                |  |    | | |||||      || |  |   |  ||     ||||   |||  | ||
Db        302 CTTTTGTCTATATTTGTATATTGAGTATATTTCCTCTTTGTAAGATTAACATTTTGTTTG 243

Qy       1188 AGAAA 1192
                | |
Db        242 TTACA 238


RESULT 12
US-09-710-279-3580/c
; Sequence 3580, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/09/710,279
;  CURRENT FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3580
;   LENGTH: 2999
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3580

  Query Match             3.6%;  Score 43.4;  DB 4;  Length 2999;
  Best Local Similarity   46.3%;  Pred. No. 0.8;
  Matches  143;  Conservative    0;  Mismatches  166;  Indels    0;  Gaps    0;

Qy        893 TGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGGTATGTA 952
              | ||| | ||   |   |||| ||       ||| | |||| | || |       |  ||
Db        458 TACAAACGGATGGTTTACTTTGCATCTATAATTTTTTCTATTGATCAACCACTATTCGTG 399

Qy        953 ATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAGCTCG 1012
              | | | | | |        ||  | |   |   ||||     | ||   | |  |
Db        398 CGCTGATAGTAAGCTAACTACATTAACCTTTTTATTTTTCCTGCAAATAATTATAAATAC 339

Qy       1013 TGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTT 1072
              | |  ||          |  || |  | |       || |  ||| || | | |  || | |
Db        338 TCTTCTATAAAAATTTAATCTACATCAATATTTTCTAATAATTAATTACGCATATAATGT 279

Qy       1073 TGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTAGTAAT 1132
              ||||| |  | |  |||  | ||  |||  || | || | ||    | || ||||   ||
Db        278 TGAAACACTTTATATTTCCATATCCATATTTTAAATTCATATTATAAATTAATTAAAGAT 219

Qy       1133 ACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAA 1192
                | | |||| |||  |||    |       | ||||  | ||   ||  | ||    |||
Db        218 CGTGATAATTTTAGTTAATACATATACTGCTTTTTATATTTTTTATTCAATTCATGAAAA 159

Qy       1193 ACAGTCTTA 1201
              |   | |||
Db        158 AATTTTTTA 150


RESULT 13
US-09-710-279-4201/c
; Sequence 4201, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/09/710,279
;  CURRENT FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4201
;   LENGTH: 3099
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-09-710-279-4201

  Query Match             3.6%;  Score 43.4;  DB 4;  Length 3099;
  Best Local Similarity   46.3%;  Pred. No. 0.8;
  Matches  143;  Conservative    0;  Mismatches  166;  Indels    0;  Gaps    0;

Qy        893 TGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGGTATGTA 952
              | ||| | ||   |   |||| ||       ||| | |||| | || |       |  ||
Db       3051 TACAAACGGATGGTTTACTTTGCATCTATAATTTTTTCTATTGATCAACCACTATTCGTG 2992

Qy        953 ATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAGCTCG 1012
              | | | | | |        ||  | |   |   ||||     | ||   | |  |
Db       2991 CGCTGATAGTAAGCTAACTACATTAACCTTTTTATTTTTCCTGCAAATAATTATAAATAC 2932

Qy       1013 TGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTT 1072
              | |  ||          |  || |  | |       || |  ||| || | | |  || | |
Db       2931 TCTTCTATAAAAATTTAATCTACATCAATATTTTCTAATAATTAATTACGCATATAATGT 2872

Qy       1073 TGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTAGTAAT 1132
              ||||| |  | |  |||  | ||  |||  || | || | ||    | || ||||   ||
Db       2871 TGAAACACTTTATATTTCCATATCCATATTTTAAATTCATATTATAAATTAATTAAAGAT 2812

Qy       1133 ACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAA 1192
                | | |||| |||  |||    |       | ||||  | ||   ||  | ||    |||
Db       2811 CGTGATAATTTTAGTTAATACATATACTGCTTTTTATATTTTTTATTCAATTCATGAAAA 2752

Qy       1193 ACAGTCTTA 1201
              |   | |||
Db       2751 AATTTTTTA 2743


RESULT 14
```

US-09-710-279-3614
; Sequence 3614, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3614
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3614

Query Match 3.6%; Score 43.4; DB 4; Length 3501;
Best Local Similarity 46.3%; Pred. No. 0.83;
Matches 143; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

```
Qy        893 TGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGGTATGTA 952
              | ||| | ||    |   |||| ||      ||| | |||| | || |        |  ||
Db       2611 TACAAACGGATGGTTTACTTTGCATCTATAATTTTTTCTATTGATCAACCACTATTCGTG 2670

Qy        953 ATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAGCTCG 1012
              | | | | | |         ||  | |   |   ||||     | ||   | |  |
Db       2671 CGCTGATAGTAAGCTAACTACATTAACCTTTTTATTTTTCCTGCAAATAATTATAAATAC 2730

Qy       1013 TGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTT 1072
              | |  ||           |  || |  | |      || |  ||| || | | |  || | |
Db       2731 TCTTCTATAAAAATTTAATCTACATCAATATTTTCTAATAATTAATTACGCATATAATGT 2790

Qy       1073 TGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTAGTAAT 1132
              ||||| |  | |  |||  | ||  |||  || | || | ||    | || |||| . ||
Db       2791 TGAAACACTTTATATTTCCATATCCATATTTTAAATTCATATTATAAATTAATTAAAGAT 2850

Qy       1133 ACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAA 1192
              | | |||| |||  |||   |       | ||||  | ||   ||  | ||    |||
Db       2851 CGTGATAATTTTAGTTAATACATATACTGCTTTTTATATTTTTTATTCAATTCATGAAAA 2910

Qy       1193 ACAGTCTTA 1201
              |   | |||
Db       2911 AATTTTTTA 2919
```

RESULT 15
US-09-710-279-3619/c
; Sequence 3619, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3619
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3619

Query Match 3.6%; Score 43.4; DB 4; Length 4015;
Best Local Similarity 46.3%; Pred. No. 0.87;
Matches 143; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

```
Qy        893 TGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGGTATGTA 952
              | ||| | ||    |   |||| ||      ||| | |||| | || |        |  ||
Db       1134 TACAAACGGATGGTTTACTTTGCATCTATAATTTTTTCTATTGATCAACCACTATTCGTG 1075

Qy        953 ATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAGCTCG 1012
              | | | | | |         ||  | |   |   ||||     | ||   | |  |
Db       1074 CGCTGATAGTAAGCTAACTACATTAACCTTTTTATTTTTCCTGCAAATAATTATAAATAC 1015

Qy       1013 TGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTT 1072
              | |  ||           |  || |  | |      || |  ||| || | | |  || | |
Db       1014 TCTTCTATAAAAATTTAATCTACATCAATATTTTCTAATAATTAATTACGCATATAATGT 955

Qy       1073 TGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTAGTAAT 1132
              |||| |  | |  |||  | ||  |||  || | || | ||    | || |||| . ||
Db        954 TGAAACACTTTATATTTCCATATCCATATTTTAAATTCATATTATAAATTAATTAAAGAT 895

Qy       1133 ACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAA 1192
              | | |||| |||  |||   |       | ||||  | ||   ||  | ||    |||
Db        894 CGTGATAATTTTAGTTAATACATATACTGCTTTTTATATTTTTTATTCAATTCATGAAAA 835

Qy       1193 ACAGTCTTA 1201
              |   | |||
Db        834 AATTTTTTA 826
```

Search completed: January 19, 2005, 17:04:40
Job time : 378 secs

GenCore version 5.1.6


OM nucleic - nucleic search, using sw model

Run on: January 18, 2005, 20:57:16 ; Search time 678 Seconds
(without alignments)
9438.118 Million cell updates/sec

Title: US-10-070-666A-1
Perfect score: 1219
Sequence: 1 agtaagcaaactaaatttaa.....taacaaaaaaaaaaaaaaaa 1219

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| | 1 | 1219 | 100.0 | 1219 | 4 | AAF61947 | Aaf61947 T. thermo |
| | 2 | 614.4 | 50.4 | 2492 | 4 | AAF61948 | Aaf61948 T. thermo |
| | 3 | 64 | 5.3 | 2000 | 8 | ADA71938 | Ada71938 Rice gene |
| | 4 | 59 | 4.8 | 8056 | 8 | ABZ10246 | Abz10246 Haematopo |
| c | 5 | 58 | 4.8 | 6103 | 6 | ABL33690 | Abl33690 Human imm |
| c | 6 | 57.4 | 4.7 | 8056 | 8 | ABZ10100 | Abz10100 Haematopo |
| c | 7 | 54.6 | 4.5 | 8056 | 8 | ABZ10246 | Abz10246 Haematopo |
| | 8 | 53.2 | 4.4 | 1501 | 8 | ABZ10188 | Abz10188 Haematopo |
| | 9 | 53.2 | 4.4 | 1501 | 10 | ADE84162 | Ade84162 Human lym |
| c | 10 | 52.6 | 4.3 | 1199 | 3 | AAA02542 | Aaa02542 Human col |
| | 11 | 52 | 4.3 | 110000 | 6 | ABA92787_0 | Aba92787 Buchnera |
| c | 12 | 51.8 | 4.2 | 424 | 8 | ABX46053 | Abx46053 Bovine ES |
| c | 13 | 51.8 | 4.2 | 7319 | 6 | ABL34044 | Abl34044 Human imm |
| c | 14 | 51.4 | 4.2 | 5728 | 6 | ABL32101 | Abl32101 Human imm |
| c | 15 | 51.2 | 4.2 | 5750 | 4 | AAS46709 | Aas46709 Tumour su |
| c | 16 | 51.2 | 4.2 | 5750 | 6 | ABL34009 | Abl34009 Human imm |
| | 17 | 50.8 | 4.2 | 3549 | 3 | AAA70223 | Aaa70223 Plasmodiu |
| | 18 | 50.4 | 4.1 | 13427 | 6 | ABL33927 | Abl33927 Human imm |
| c | 19 | 50 | 4.1 | 8951 | 6 | ABL32795 | Abl32795 Human imm |
| | 20 | 50 | 4.1 | 16439 | 6 | ABL32887 | Abl32887 Human imm |
| c | 21 | 49.8 | 4.1 | 5442 | 6 | ABL33969 | Abl33969 Human imm |
| c | 22 | 49.8 | 4.1 | 10328 | 6 | ABL33544 | Abl33544 Human imm |
| c | 23 | 49.4 | 4.1 | 2000 | 6 | ABZ15104 | Abz15104 Arabidops |
| | 24 | 49.4 | 4.1 | 2000 | 6 | ABZ14950 | Abz14950 Arabidops |
| c | 25 | 49.4 | 4.1 | 7676 | 6 | ABL34598 | Abl34598 Human met |
| c | 26 | 49.4 | 4.1 | 7676 | 6 | ABL70409 | Abl70409 Chemicall |
| | 27 | 49 | 4.0 | 8056 | 8 | ABZ10100 | Abz10100 Haematopo |
| c | 28 | 48.8 | 4.0 | 1830 | 6 | ABL56243 | Abl56243 AmEPV met |
| | 29 | 48.8 | 4.0 | 32392 | 6 | ABL56203 | Abl56203 AmEPV gen |
| c | 30 | 48.6 | 4.0 | 6129 | 6 | ABL34582 | Abl34582 Human met |
| | 31 | 48 | 3.9 | 1501 | 8 | ABZ10042 | Abz10042 Haematopo |
| | 32 | 48 | 3.9 | 1501 | 10 | ADE84086 | Ade84086 Human lym |
| | 33 | 47.8 | 3.9 | 1348 | 4 | AAH74716 | Aah74716 Nucleotid |
| c | 34 | 47.8 | 3.9 | 16724 | 6 | ABL33091 | Abl33091 Human imm |
| c | 35 | 47.8 | 3.9 | 16724 | 6 | ABL34537 | Abl34537 Human met |
| c | 36 | 47.8 | 3.9 | 16724 | 6 | ABL70260 | Abl70260 Chemicall |
| c | 37 | 47.6 | 3.9 | 16724 | 6 | ABL33090 | Abl33090 Human imm |
| c | 38 | 47.6 | 3.9 | 16724 | 6 | ABL34536 | Abl34536 Human met |
| c | 39 | 47.6 | 3.9 | 16724 | 6 | ABL70259 | Abl70259 Chemicall |
| c | 40 | 47.4 | 3.9 | 17421 | 4 | AAS45349 | Aas45349 Chemicall |
| c | 41 | 47.4 | 3.9 | 17421 | 6 | ABK28182 | Abk28182 DNA trans |
| c | 42 | 47.4 | 3.9 | 19634 | 8 | ABZ10162 | Abz10162 Haematopo |
| c | 43 | 47.2 | 3.9 | 6749 | 4 | AAS46525 | Aas46525 Tumour su |
| c | 44 | 47.2 | 3.9 | 17703 | 6 | ABK39953 | Abk39953 Human che |
| c | 45 | 47 | 3.9 | 2000 | 8 | ADA71938 | Ada71938 Rice gene |

ALIGNMENTS

RESULT 1
AAF61947
ID AAF61947 standard; cDNA; 1219 BP.
XX
AC AAF61947;
XX
DT 22-AUG-2001 (first entry).
XX
DE T. thermophila delta-6-desaturase cDNA.
XX
KW Delta-6-desaturase; antirheumatic; antiarthritic; antiarteriosclerotic;
KW antidiabetic; neuroleptic; dermatological; gene therapy; ciliate;
KW delta-6-unsaturated fatty acid production; gamma-linolenic acid; GLA;
KW eicosanoid biosynthesis; prostaglandin; atopic eczema; atherosclerosis;
KW rheumatoid arthritis; diabetic neuropathy; schizophrenia; cosmetic;
KW animal nutrition; human nutrition; stearidonic acid;
KW plant transformation; oilseed crop; ss.
XX
OS Tetrahymena thermophila.
XX
FH Key Location/Qualifiers
FT CDS 11. .1091
FT /*tag= a
FT /product= "delta-6-desaturase"
FT /note= "contains in-frame stop codons"
FT /transl_except= (pos:51. .53, aa:Gln)
FT /transl_except= (pos:201. .203, aa:Gln)
FT /transl_except= (pos:240. .242, aa:Gln)
FT /transl_except= (pos:285. .287, aa:Gln)
FT /transl_except= (pos:633. .635, aa:Gln)
FT /transl_except= (pos:654. .656, aa:Gln)
FT /transl_except= (pos:759. .761, aa:Gln)
FT /transl_except= (pos:951. .953, aa:Gln)
FT /transl_except= (pos:957. .959, aa:Gln)
FT /transl_except= (pos:981. .983, aa:Gln)
XX
PN DE10044468-A1.
XX
PD 15-MAR-2001.
XX
PF 08-SEP-2000; 2000DE-01044468.
XX
PR 10-SEP-1999; 99DE-01043270.
XX

PA (AXIV-) AXIVA GMBH.
XX
DR WPI; 2001-245832/26.
DR P-PSDB; AAB70934.
XX
PT New nucleic acid encoding delta-6-desaturase, useful for producing
PT ciliates and plants that overproduce unsaturated fatty acids, derived
PT from Tetrahymena.
XX
PS Claim 1; Page 13; 30pp; German.
XX
CC This invention describes a novel nucleic acid (I) encoding a delta-6-
CC desaturase from Tetrahymena thermophila. The products of the invention
CC have antirheumatic, antiarthritic, antiarteriosclerotic, antidiabetic,
CC neuroleptic and dermatological and can be used for gene therapy. (I) is
CC overexpressed in ciliates to increase production of delta-6-unsaturated
CC fatty acids, specifically gamma-linolenic acid (GLA) which is an
CC intermediate in biosynthesis of eicosanoids (and e.g. prostaglandins) and
CC useful for treating e.g. atopic eczema, rheumatoid arthritis,
CC atherosclerosis, diabetic neuropathy, schizophrenia and in cosmetics and
CC in animal or human nutrition. Also production of stearidonic acid is
CC increased. (I) may also be used to transform plants, particularly oilseed
CC crops, optionally in combination with other desaturases. Fragments of (I)
CC are useful for producing individual epitopes, and as probes for
CC identifying related sequences, as antisense sequences and as primers for
CC polymerase chain reaction. The desaturase, or its fragments, can be used
CC to raise antibodies, used e.g. to isolate homologous proteins.
CC Tetrahymena transformed with (I) are easy to grow on a large scale and at
CC high cell density, without being affected by weather and environmental
CC pollutants. They produce a pattern of fatty acids far simpler than that
CC produced by higher organisms. This cDNA sequence encodes the Tetrahymena
CC thermophila delta-6-desaturase protein described in the method of the
CC invention
XX
SQ Sequence 1219 BP; 420 A; 204 C; 182 G; 413 T; 0 U; 0 Other;

Query Match 100.0%; Score 1219; DB 4; Length 1219;
Best Local Similarity 100.0%; Pred. No. 1.8e-227;
Matches 1219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGTAAGCAAACTAAATTTAAAAAACAAGCATTATGGGAGTTGATAAGACTTAAGAAGAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGTAAGCAAACTAAATTTAAAAAACAAGCATTATGGGAGTTGATAAGACTTAAGAAGAAA 60

Qy         61 TTGTTCTTGAAAATAAACCCGAACTTCTCAACGAATACAAATTTATTTACAAGGATACTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGTTCTTGAAAATAAACCCGAACTTCTCAACGAATACAAATTTATTTACAAGGATACTG 120

Qy        121 AATATGACTGCACTGAATATGCTAAATCAAATAAGCATCCTGGCGGTCTTAATTTCCTCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AATATGACTGCACTGAATATGCTAAATCAAATAAGCATCCTGGCGGTCTTAATTTCCTCA 180

Qy        181 ATTTGTTTATTGATGAGAAGTAAGATTTGACTGAATATTTCAGAACACTCCATTCTAAGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATTTGTTTATTGATGAGAAGTAAGATTTGACTGAATATTTCAGAACACTCCATTCTAAGT 240

Qy        241 AGGCTTTGAAAATTTTAAAATCCTTCCCTAAGACTGGCGCAAAATAAGAGGAGACTGAAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGCTTTGAAAATTTTAAAATCCTTCCCTAAGACTGGCGCAAAATAAGAGGAGACTGAAT 300

Qy        301 CTTCAAAGAGATTCTCAATATTAAAGAAAAAGCTTAAGCATTTATTCGAACCAAACTGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTCAAAGAGATTCTCAATATTAAAGAAAAAGCTTAAGCATTTATTCGAACCAAACTGGC 360

Qy        361 CTATCGAAATTGGTTTATTCTTAACTACCTTTACTTTATTTGTCACTGGATGTTTGACTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTATCGAAATTGGTTTATTCTTAACTACCTTTACTTTATTTGTCACTGGATGTTTGACTC 420

Qy        421 AAAAGTGGTATTTCTCTATTCCCCTTCTTGTCTTAATGCAAATCATCAGTGGTTGGATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAAAGTGGTATTTCTCTATTCCCCTTCTTGTCTTAATGCAAATCATCAGTGGTTGGATTG 480

Qy        481 GTCACTCTATGAACCACAATCGTAACCCTATATTAAGAAAATTCGCTTTAGTCTACGCTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTCACTCTATGAACCACAATCGTAACCCTATATTAAGAAAATTCGCTTTAGTCTACGCTC 540

Qy        541 CTCTTTGTGGTGGTTTCTCTAATAAATGGTGGGGTAGGAAGCACAATCAACATCATATGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTCTTTGTGGTGGTTTCTCTAATAAATGGTGGGGTAGGAAGCACAATCAACATCATATGT 600

Qy        601 TCACAAACAACATTCTAAAGGACGAAGATATCTAACACGATTACAAATTGTGGTAATTCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCACAAACAACATTCTAAAGGACGAAGATATCTAACACGATTACAAATTGTGGTAATTCC 660

Qy        661 CCTTCTTATTTTTAAAGTGGAAATTAGACTCCATCTTAGCTTCTTATTATGAATTTGAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCTTCTTATTTTTAAAGTGGAAATTAGACTCCATCTTAGCTTCTTATTATGAATTTGAAG 720

Qy        721 GAATCTTCCTTGCCTTGCACTGGGTATTATTATTCAACTAAAACTTCTATATCGTAATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAATCTTCCTTGCCTTGCACTGGGTATTATTATTCAACTAAAACTTCTATATCGTAATTC 780

Qy        781 TTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTGGAAATCATGAAAATG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTGGAAATCATGAAAATG 840

Qy        841 AAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCAAATAGCTGCAAGCA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCAAATAGCTGCAAGCA 900

Qy        901 GAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGGTATGTAATATTAGA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGGTATGTAATATTAGA 960

Qy        961 CTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAGCTCGTGTCATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAGCTCGTGTCATAA 1020

Qy       1021 TTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTTTGAAAAAT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTTTGAAAAAT 1080

Qy       1081 CTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTAGTAATACTAACAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTAGTAATACTAACAA 1140

Qy       1141 TTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAAACAGTCTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAAACAGTCTT 1200

Qy       1201 AACAAAAAAAAAAAAAAAA 1219
              ||||||||||||||||||||
Db       1201 AACAAAAAAAAAAAAAAAA 1219
```

RESULT 2
AAF61948
ID AAF61948 standard; DNA; 2492 BP.
XX
AC AAF61948;
XX
DT 22-AUG-2001 (first entry)
XX
DE T. thermophila delta-6-desaturase genomic DNA.
XX
KW Delta-6-desaturase; antirheumatic; antiarthritic; antiarteriosclerotic;
KW antidiabetic; neuroleptic; dermatological; gene therapy; ciliate;
KW delta-6-unsaturated fatty acid production; gamma-linolenic acid; GLA;
KW eicosanoid biosynthesis; prostaglandin; atopic eczema; atherosclerosis;
KW rheumatoid arthritis; diabetic neuropathy; schizophrenia; cosmetic;
KW animal nutrition; human nutrition; stearidonic acid;
KW plant transformation; oilseed crop; ds.
XX
OS Tetrahymena thermophila.
XX
PN DE10044468-A1.

XX
PD 15-MAR-2001.
XX
PF 08-SEP-2000; 2000DE-01044468.
XX
PR 10-SEP-1999; 99DE-01043270.
XX
PA (AXIV-) AXIVA GMBH.
XX
DR WPI; 2001-245832/26.
XX
PT New nucleic acid encoding delta-6-desaturase, useful for producing
PT ciliates and plants that overproduce unsaturated fatty acids, derived
PT from Tetrahymena.
XX
PS Example 6; Page 15-16; 30pp; German.
XX
CC This invention describes a novel nucleic acid (I) encoding a delta-6-
CC desaturase from Tetrahymena thermophila. The products of the invention
CC have antirheumatic, antiarthritic, antiarteriosclerotic, antidiabetic,
CC neuroleptic and dermatological and can be used for gene therapy. (I) is
CC overexpressed in ciliates to increase production of delta-6-unsaturated
CC fatty acids, specifically gamma-linolenic acid (GLA) which is an
CC intermediate in biosynthesis of eicosanoids (and e.g. prostaglandins) and
CC useful for treating e.g. atopic eczema, rheumatoid arthritis,
CC atherosclerosis, diabetic neuropathy, schizophrenia and in cosmetics and
CC in animal or human nutrition. Also production of stearidonic acid is
CC increased. (I) may also be used to transform plants, particularly oilseed
CC crops, optionally in combination with other desaturases. Fragments of (I)
CC are useful for producing individual epitopes, and as probes for
CC identifying related sequences, as antisense sequences and as primers for
CC polymerase chain reaction. The desaturase, or its fragments, can be used
CC to raise antibodies, used e.g. to isolate homologous proteins.
CC Tetrahymena transformed with (I) are easy to grow on a large scale and at
CC high cell density, without being affected by weather and environmental
CC pollutants. They produce a pattern of fatty acids far simpler than that
CC produced by higher organisms. This DNA sequence encodes the Tetrahymena
CC thermophila delta-6-desaturase protein described in the method of the
CC invention
XX
SQ Sequence 2492 BP; 952 A; 331 C; 309 G; 900 T; 0 U; 0 Other;

Query Match 50.4%; Score 614.4; DB 4; Length 2492;
Best Local Similarity 99.8%; Pred. No. 5.3e-110;
Matches 615; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       589 AACATCATATGTTCACAAACAACATTCTAAAGGACGAAGATATCTAACACGATTACAAAT 648
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1652 AGCATCATATGTTCACAAACAACATTCTAAAGGACGAAGATATCTAACACGATTACAAAT 1711

Qy       649 TGTGGTAATTCCCCTTCTTATTTTTAAAGTGGAAATTAGACTCCATCTTAGCTTCTTATT 708
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1712 TGTGGTAATTCCCCTTCTTATTTTTAAAGTGGAAATTAGACTCCATCTTAGCTTCTTATT 1771

Qy       709 ATGAATTTGAAGGAATCTTCCTTGCCTTGCACTGGGTATTATTATTCAACTAAAACTTCT 768
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1772 ATGAATTTGAAGGAATCTTCCTTGCCTTGCACTGGGTATTATTATTCAACTAAAACTTCT 1831

Qy       769 ATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTGGAA 828
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1832 ATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTGGAA 1891

Qy       829 ATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCAAA 888
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1892 ATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCAAA 1951

Qy       889 TAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGGTA 948
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1952 TAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGGTA 2011

Qy       949 TGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAG 1008
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Db      2012 TGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAG 2071

Qy       1009 CTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTA 1068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2072 CTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTA 2131

Qy       1069 TTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTAG 1128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2132 TTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTAG 2191

Qy       1129 TAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGA 1188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2192 TAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGA 2251

Qy       1189 GAAAACAGTCTTAACA 1204
              ||||||||||||||||
Db       2252 GAAAACAGTCTTAACA 2267
```

RESULT 3
ADA71938
ID ADA71938 standard; DNA; 2000 BP.
XX
AC ADA71938;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 5263.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX
OS Oryza sativa.
XX
PN WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 27; SEQ ID NO 5263; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

Query Match 5.3%; Score 64; DB 8; Length 2000;
Best Local Similarity 10.9%; Pred. No. 0.0043;
Matches 89; Conservative 362; Mismatches 357; Indels 8; Gaps 2;

```
Qy       103 TTATTTACAAGGATACTGAATATGACTGCACTGAATATGCTAAATCAAATAAGCATCCTG 162
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Db        220 KYGTYKKMTYYSASRCMRAYMTTSYSWACSSYTWCRSKRRSMMWKMMRKMRWSRSYGWYS 279

Qy        163 GCGGTCTTAATTTCCTCAATTTGTTTATTGATGAGAAGTAAGATTTGACTGAATATTTCA 222

Db        280 WSYKMWMCTAYKKSYYSRWCYMYRGGGWRGATRYWGRGYMSRMAMMYKKMYWYRGYKGMK 339

Qy        223 GAACACTCCATTCTAAGTAGGCTTTGAAAATTTTAAAATCCTTCCCTAAGACTGGCGCAA 282

Db        340 RGWWAGRMMMRSMCRWSKACYYMRWRMWRMTRRRRWAKKSSRTSRRKKRKWCMRKRKYKR 399

Qy        283 AA---TAAGAGGAGACTGAATCTTCAAAGAGATTCTCAATATTAAAGAAAAAGCTTAAGC 339

Db        400 MRGYSRMRSCKRARWMKRCRSGRAWKMGCRGCMTCRMKSYGMMRWKSWKRMASKYKWMSR 459

Qy        340 ATTTATTCGAACCAAACTGGCCTATCGAAATTGGTTTATTCTTAACTACCTTTACTTTAT 399

Db        460 MYRWRKKKCSRTTMWGKTRGGMMGTMGRCRYKKRSGMKRKCRRRRWGRMYRMRWKRYYMS 519

Qy        400 TTGTCACTGGATGTTTGACTCAAAAGTGGTATTTCTCTATTCCCCTTCTTGTCTTAATGC 459

Db        520 ARYTMRYCARKKYSYSAARKARCWYRGKGYYWAGMWMKRYKRMYMYKMMWWYKRKYSKCS 579

Qy        460 AAATCATCAGTGGTTGGATTGGTCACTCTATGAACCACAATCGTAACCCTATATTAAGAA 519

Db        580 WYCKMSYYASCMKSARKAGAKMCKRSKMSAWSKSMRSSRKCRKCASKRSSAKRYAMMGGM 639

Qy        520 AATTCGCTTTAGTCTACGCTCCTCTTTGTGGTGGTTTCTCTAATAAATGGTGGGGTAGGA 579

Db        640 TSGSRMSRWKSYTCYWRKWGSMKSTCTWMYYMSKYTYAKYGSYWRYRYRAWCMYMWRWYY 699

Qy        580 AGCACAATCAACATC-----ATATGTTCACAAACAACATTCTAAAGGACGAAGATATCTA 634

Db        700 YRYRSYMTYMAWYTSSTRMAMTGMKYSGRYWTSWYKYCKCSWKYRSMWYYWSWWWAKTWK 759

Qy        635 ACACGATTACAAATTGTGGTAATTCCCCTTCTTATTTTTAAAGTGGAAATTAGACTCCAT 694

Db        760 MWRRYATRMMWMWYRYSMKWYTWCTMWGYWWYWWRTYMKMRYMWYKCTKTYWYWSATYWT 819

Qy        695 CTTAGCTTCTTATTATGAATTTGAAGGAATCTTCCTTGCCTTGCACTGGGTATTATTATT 754

Db        820 GTWAAWWMAKTKMRMGMTGAKTRGRARKARYWWKWATWCATKRWMTKGKGAKWAWTWMAK 879

Qy        755 CAACTAAAACTTCTATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTC 814

Db        880 AWRKYYWSWMRAWYYYYKTRRTRYKTCWWKARWGSWAYWRMWWKGSAKMWWMWKGGRWGW 939

Qy        815 TATTCTTGTTGGAAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATT 874

Db        940 TKYWYWYCTTWKMACGRATKYMCCAGWWAMYSYSWTRTYWMRTWRWMWASSRTAKRMARM 999

Qy        875 TTTCGAACATCAAATAGCTGCAAGCAGAAACTACGC 910

Db       1000 MWKTRAWSKSYARAYWKMAGCACCTACACACTACAC 1035
```

RESULT 4
ABZ10246
ID ABZ10246 standard; DNA; 8056 BP.
XX
AC ABZ10246;
XX
DT 16-JAN-2003 (first entry)
XX
DE Haematopoietic cell proliferation disorder related DNA sequence #386.
XX
KW Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200277272-A2.

XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-EP003401.
XX
PR 26-MAR-2001; 2001US-0278333P.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwope I, Ziebarth H;
XX
DR WPI; 2003-018942/01.
XX
PT Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS Claim 28; SEQ ID NO 386; 117pp; English.
XX
CC The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
SQ Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;

Query Match 4.8%; Score 59; DB 8; Length 8056;
Best Local Similarity 44.3%; Pred. No. 0.047;
Matches 483; Conservative 0; Mismatches 585; Indels 23; Gaps 5;

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Qy        101 ATTTATTTACAAGGATACTGAATATGACTGCACTGAATATGCTAAATCAAATAAGCATCC 160

Db       2396 ATTTTTTGAAAATTAAAAAAAAAAATAATTTATTTATTTTTAAAAATTAATTTTTTTTTAT 2455

Qy        161 TGGCGGTCTTAATTTCCTCAATTTGTTTATTGATGAGAAGTAAGATTTGACTGAATATTT 220

Db       2456 TTTTATTTATATATTTTTTATTATTTTGTTTTAAAATAATTAAAATATTAATGAAAAATA 2515

Qy        221 CAGA-----ACACTCCATTCTAAGTAGGCTTTGAAAATTTTAAAATCCTTCCCTAAGACT 275

Db       2516 AAAAAAAATAAATTAAATTATAAAATAAATTAAAAAATTTAAAAATTTAAATAAAATTTT 2575

Qy        276 GGCGCAAAATAAGAGGAGACTGAATCTTCAAAGAGATTCTCAATATTAAAGAAAAAGCTT 335

Db       2576 TAAAAAATAAAAAATAAATGAAAAAAAAAATTATAAATATAAATAATTTAAAAAAAAAAA 2635

Qy        336 AAGCATTTATTCGAACCAAACTGGCCTATCGAAATTGGTTTATTCTTAACTACCTTTACT 395

Db       2636 ATAAAAAAAAATGTTAAAATTTAAAATTTAAAAATAATAAATTTTTAAATTTTTTTAAA 2695

Qy        396 TTATTTGTCACTGGATGTTTGACTCAAAAGTGGTATTTCTCTATTCCCCTTCTTGTCTTA 455
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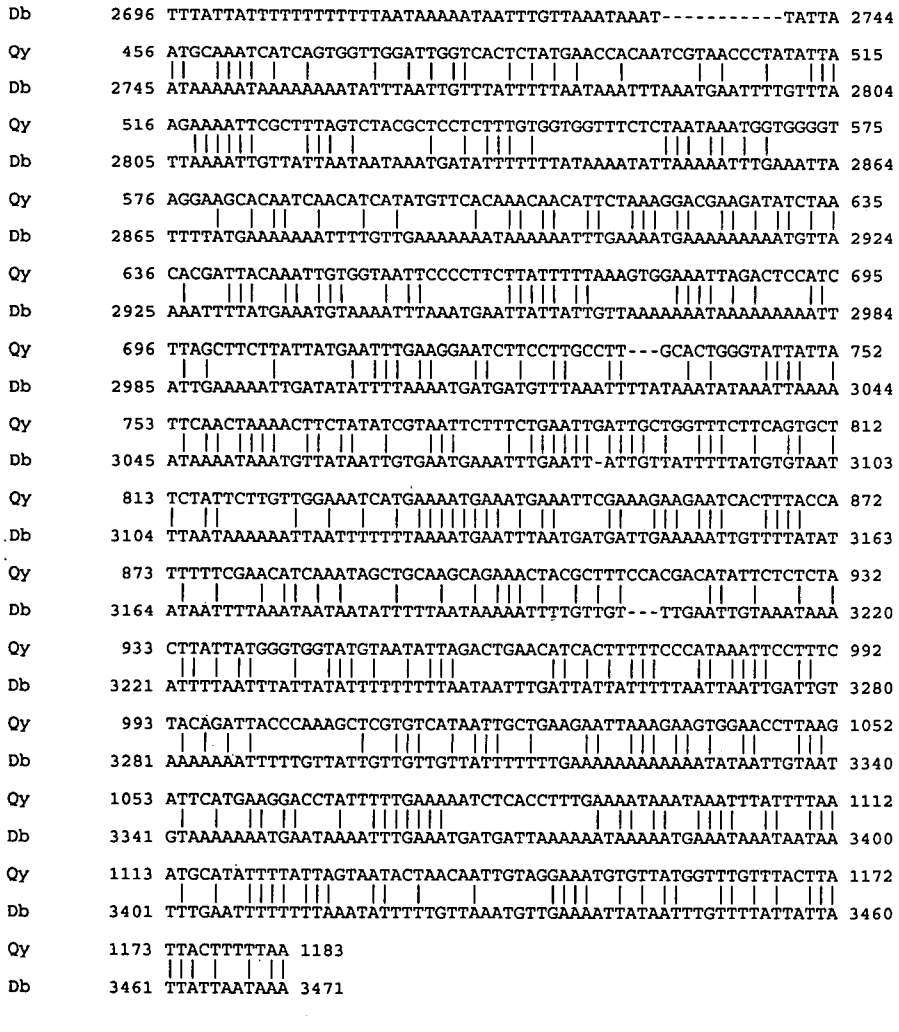
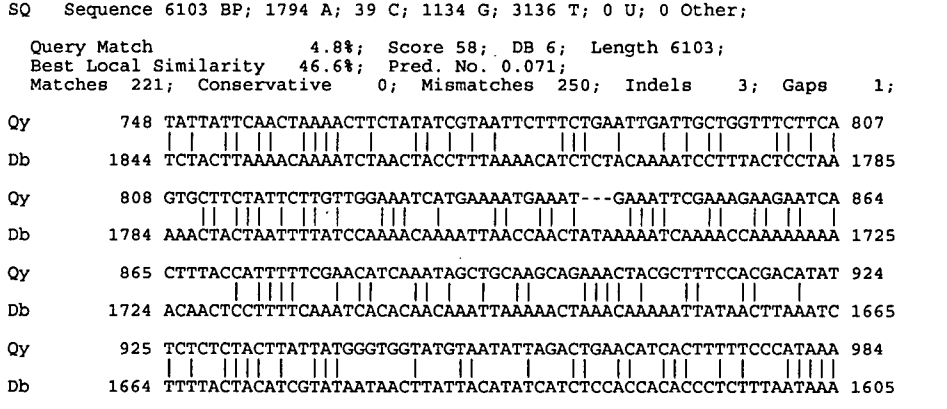


RESULT 5
ABL33690/c
ID ABL33690 standard; DNA; 6103 BP.
XX
AC ABL33690;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 1663.
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW ds.
XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP007537.
XX
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.
XX
PS Claim 1; SEQ ID NO 1663; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX
SQ Sequence 6103 BP; 1794 A; 39 C; 1134 G; 3136 T; 0 U; 0 Other;

Query Match 4.8%; Score 58; DB 6; Length 6103;
Best Local Similarity 46.6%; Pred. No. 0.071;
Matches 221; Conservative 0; Mismatches 250; Indels 3; Gaps 1;



RESULT 6

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ABZ10100/c
ID   ABZ10100 standard; DNA; 8056 BP.
XX
AC   ABZ10100;
XX
DT   16-JAN-2003  (first entry)
XX
DE   Haematopoietic cell proliferation disorder related DNA sequence #240.
XX
KW   Human; haematopoietic cell proliferation disorder; cytostatic;
KW   gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW   cytosine methylation state; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200277272-A2.
XX
PD   03-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-EP003401.
XX
PR   26-MAR-2001; 2001US-0278333P.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Berlin K,  Braun A,  Distler J,  Guetig D,  Howe A,  Mueller J;
PI   Olek A,  Piepenbrock C,  Adorjan P,  Grabs G,  Lesche R,  Leu E;
PI   Lewin A,  Lipscher E,  Maier S,  Model F,  Mueller V,  Otto T,  Pelet C;
PI   Schwope I,  Ziebarth H;
XX
DR   WPI; 2003-018942/01.
XX
PT   Detecting and differentiating between hematopoietic cell proliferative
PT   disorders, comprises contacting a target nucleic acid with a reagent that
PT   distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS   Claim 28; SEQ ID NO 240; 117pp; English.
XX
CC   The present invention describes a method for detecting and
CC   differentiating between haematopoietic cell proliferative disorders
CC   associated with at least 1 gene and/or their regulatory regions in a
CC   subject. The method comprises contacting a target nucleic acid in a
CC   biological sample obtained from the subject with at least 1 reagent,
CC   which distinguishes between methylated and non-methylated CpG
CC   dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC   represent specifically claimed nucleotide sequences from the present
CC   invention. Oligonucleotides from the present invention can be used: for
CC   differentiating between healthy haematopoietic cells and proliferative
CC   disorder haematopoietic cells; for differentiating between acute
CC   lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC   determining the cytosine methylation state and/or single nucleotide
CC   polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC   related sequences and their complements; and as primers for the
CC   amplification of haematopoietic cell proliferation disorder related DNA
CC   sequences. The nucleotide sequences from the present invention can also
CC   be used for detecting a predisposition to, differentiation between
CC   subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC   haematopoietic cell proliferative disorders. The present method enables a
CC   highly specific classification of haematopoietic cell proliferative
CC   disorders allowing for improved and informed treatment of patients
XX
SQ   Sequence 8056 BP; 3711 A; 371 C; 371 G; 3603 T; 0 U; 0 Other;

  Query Match             4.7%;  Score 57.4;  DB 8;  Length 8056;
  Best Local Similarity   44.3%;  Pred. No. 0.096;
  Matches  283;  Conservative    0;  Mismatches  351;  Indels    5;  Gaps    1;

Qy        586 ATCAACATCATATGTTCACAAACAACATTCTAAAGGACGAAGATATCTAACACGATTACA 645
              || || |   ||| |    ||  |   || | ||  |  || |    |||    |  | |
Db       2746 ATTAATAATTTATTTAACGAATTATTTTTATTAAAAAAAAAAAATAATAAATTTAAAAAA 2687

Qy        646 AATTGTGGTAATTCCCCTTCTTATTTTTAAAGTGGAAATTAGACTCCATCTTAGCTTCTT 705
                | ||       |     || | |  ||| || |   ||       |   | ||   || ||

Db       2686 ATTTAAAAATTTATTATTTTTAAAATTTTAAATTTTAACGTTTTTTTTTATTTTTTTTT 2627

Qy        706 ATTATGAATTTGAAGGAATCTTCCTTGCCTTGCACTGGGTATTATTATTCAACTAAAACT 765
              | |   |||| |   ||  |  ||   ||     |   | ||||| || ||  |
Db       2626 TTAAATTATTTATATTTATAATTTTTTTTTCGTTTATTTTTTATTTTTTAAAAATTTTA 2567

Qy        766 TCTATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTG 825
              | || ||  | |   ||| | | ||  ||  |  ||| |   |  | | | ||  | |
Db       2566 TTTAAATTTTTAAATTTTTTAATTTATTTTATAATTTAATTTATTTTTTTTTATTTTTCG 2507

Qy        826 GAAA-----TCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGA 880
                ||      | || |   | ||| |||||   ||| || |   |  | |  ||      |
Db       2506 TTAATATTTTAATTATTTTAAAACGAAATAATAAAAAATATATAAATAAAAATAAAAAAA 2447

Qy        881 ACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTAT 940
              |  | | |       |   | ||| ||   |||      |  |         || | |   |
Db       2446 AATTAATTTTTAAAAATAAATAAATTATTTTTTTTTTAATTTTCGAAAAATAATAAAATT 2387

Qy        941 GGGTGGTATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATT 1000
                |   | |     | |   || || |  |||     || || |    | ||    |
Db       2386 TAATAAATTATTTATAAAAATAAAAAATTATATTTAAAAATTAAATAAAATTTATTTAAA 2327

Qy       1001 ACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGA 1060
              | |||  |  |    || ||    || || ||||  |    |    |  ||
Db       2326 TACGAAAATTAATAAATTATTTTAAAAATAAATAAATTAAAAAATTAAAATTTTTTAAT 2267

Qy       1061 AGGACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATAT 1120
                 ||  | | |||||    |  |||   || |   || ||| ||||   |  || |
Db       2266 TTATTTTAAATATTAAAAAATAAATTTTTATTAAAATTAAATTTTTTTTTTTTTTATTT 2207

Qy       1121 TTTATTAGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTT 1180
              ||| ||      | | | | || ||  |||  | | ||  ||| |||  |||||  | |
Db       2206 TTTTTTTCGTTTTTTTAAATTTTTAATAAAATTATAATTTTTTTTTTTTTTATTTTTTAT 2147

Qy       1181 TAATCTGAGAAAACAGTCTTAACAAAAAAAAAAAAAAAA 1219
              |  |   | || | |   |||  ||||  | |  ||| |
Db       2146 TTTTAATAAAATAAAAAATTATTAAAATTATATTAAATA 2108


RESULT 7
ABZ10246/c
ID   ABZ10246 standard; DNA; 8056 BP.
XX
AC   ABZ10246;
XX
DT   16-JAN-2003  (first entry)
XX
DE   Haematopoietic cell proliferation disorder related DNA sequence #386.
XX
KW   Human; haematopoietic cell proliferation disorder; cytostatic;
KW   gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW   cytosine methylation state; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200277272-A2.
XX
PD   03-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-EP003401.
XX
PR   26-MAR-2001; 2001US-0278333P.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Berlin K,  Braun A,  Distler J,  Guetig D,  Howe A,  Mueller J;
PI   Olek A,  Piepenbrock C,  Adorjan P,  Grabs G,  Lesche R,  Leu E;
PI   Lewin A,  Lipscher E,  Maier S,  Model F,  Mueller V,  Otto T,  Pelet C;
PI   Schwope I,  Ziebarth H;
XX
DR   WPI; 2003-018942/01.
XX
PT   Detecting and differentiating between hematopoietic cell proliferative
```

PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS Claim 28; SEQ ID NO 386; 117pp; English.
XX
CC The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
SQ Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;

Query Match 4.5%; Score 54.6; DB 8; Length 8056;
Best Local Similarity 45.3%; Pred. No. 0.33;
Matches 282; Conservative 0; Mismatches 334; Indels 7; Gaps 2;

```
Qy       596 TATGTTCACAAACAACATTCTAAAGGACGAAGATATCTAACACGATTACAAATTGTGGTA 655
Db      6415 TATATATATATAATATATAATATATAATTTTTTTTAATAAATATAATAAAAATTTATTTA 6356

Qy       656 ATTCCCCTTCTTATTTTTAAAGTGGAAATTAGACTCCATCTTAGCTTCTTATTATGAATT 715
Db      6355 TAACACATTTTTTAAATATACATAATAATACATTATTAAATTATTTTAATTATTTTAAAT 6296

Qy       716 TGAAGGAATCTTCCTTGCCTTGCACTGGGTATTATTATTCAACTAAAACTTCTATATCGT 775
Db      6295 ATCATTTTTTTTTTTATATTTTTATTATTTTTTTTTATTTATATTAATATTTTACATTTT 6236

Qy       776 AATTCTTTCTGAATT--GATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTGGAAATCAT 833
Db      6235 AAACACACATTTATTAATATTTTTTTTTTTTTTATTTTTTTTAAAATTTTTAATTAAAAC 6176

Qy       834 GAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCAAATAGCT 893
Db      6175 ACAATTTTTTTTTTAATTTTAACAAAACATTTTATAATTTAATACACACATAACATAACA 6116

Qy       894 GCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGGTATGTAA 953
Db      6115 ATAAACACATAATACATTTTCAATATAAAAAATAATTATTTCATTTACAATAATTTATAT 6056

Qy       954 TATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAGCTCGT 1013
Db      6055 TTATAAAATAAAAATACAATTTATTAAATAATATTATTACAAAAAAATAATAAAAAAAAA 5996

Qy      1014 GTCATAATTGCTGAAGAATTAAAGA-----AGTGGAACCTTAAGATTCATGAAGGACCTA 1068
Db      5995 AAAAAAATTTAAAAAAAAATAAAAAAAAATAATAAACACACATAATTAATTTATACAATT 5936

Qy      1069 TTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTAG 1128
Db      5935 TTTTTATTTTATTTATATTTTAAAATTAAAATATTCAATTATTCAATTAAATTTTTTTTT 5876

Qy      1129 TAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGA 1188
Db      5875 TATTTTTTTTATTTTTTTTATTTTTTTTATAAACATTTTTTTCAAATTTTTAAAATAAAA 5816
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Qy      1189 GAAAACAGTCTTAACAAAAAAAA 1211
Db      5815 AACATAAAAAAAAAAAAAAAAAA 5793
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RESULT 8
ABZ10188
ID ABZ10188 standard; DNA; 1501 BP.
XX
AC ABZ10188;
XX
DT 16-JAN-2003 (first entry)
XX
DE Haematopoietic cell proliferation disorder related DNA sequence #328.
XX
KW Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200277272-A2.
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-EP003401.
XX
PR 26-MAR-2001; 2001US-0278333P.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwope I, Ziebarth H;
XX
DR WPI; 2003-018942/01.
XX
PT Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS Claim 28; SEQ ID NO 328; 117pp; English.
XX
CC The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
SQ Sequence 1501 BP; 604 A; 0 C; 130 G; 767 T; 0 U; 0 Other;

Query Match 4.4%; Score 53.2; DB 8; Length 1501;
Best Local Similarity 46.1%; Pred. No. 0.52;
Matches 259; Conservative 0; Mismatches 293; Indels 10; Gaps 2;

```
Qy        663 TTCTTATTTTTAAAGTGGAAATTAGACTCCATCTTAGCTTCTTATTATGAATTTGAAGGA 722
              ||  |  |||| || |  |||||  | |  || ||    | |  |||   |||||  |
Db        900 TTAATGATTTTTAATTTTAAATTTAAATTAATTTTGATGTTTGTTTAATTATTTGTTGAT 959

Qy        723 ATCTTCCTTGCCTTGCACTGGGTATTATTATTCAACTAAAACTTCTATATCGTAATTCTT 782
               | ||  ||   ||  |     ||   |||   ||      |  |  | ||  | |   ||
Db        960 TTGTTTTTTAAATTTAATAATTTAAATTTAAATAATATTGAAATGAAAATTTTGAAATTT 1019

Qy        783 TCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTGGAAATCATGAAAATGAA 842
                  |  | ||    ||| || | |  |  | || ||     | |  || ||||   |
Db       1020 AAAATTTGAAATGTAATTTTTTTAAATTTTAATTTTATT----TATAAAATAAAAAAATA 1075

Qy        843 ATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCAAATAGCTGCAAGCAGA 902
              || | |||       |  ||    ||    | ||||  || |  ||| |  |  ||  | |
Db       1076 ATAATATTTATTTTATAAAATTATTATAAAATTTTAAAAAAATAAAAATATTTAAAAAAA 1135

Qy        903 AACTACGCTTTCCACGACATATTCTCTCTACTT------ATTATGGGTGGTATGTAATAT 956
              || |    |||  |  | | | |   |    ||      ||| | | |    |   |||
Db       1136 AAATTTAATTTAAATAAAAAAATAAATGATGTTAATTTAATTTTTGTTTTAAAAAAATGA 1195

Qy        957 TAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAGCTCGTGTC 1016
              || |   |  |  | |||||   | ||     ||  |  | |||    | |  |  | |
Db       1196 TATAAAAATAAAAAATTTTTTTTAAAATAAAATTAATTAAAATTTGTTATATTTTTTTTT 1255

Qy       1017 ATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTTTGAA 1076
              ||  |   | ||  |||| | || |   |   ||| |   |  ||     |||||   ||
Db       1256 ATTTTATATAAAATATTATAAAAATTATATAATAAAAAATAAAAATTTAATATTTAAAAA 1315

Qy       1077 AAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTAGTAATACTA 1136
              | ||   |   || ||      |||||||  ||| |    ||   |||  |  |  | ||
Db       1316 ATATTATAAAATTAAATTATTTTAAATTTTATTTTATATTATTAATTAAAATAATAAATA 1375

Qy       1137 ACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAAACAG 1196
              |   || ||   ||| | || |      ||||  |||   || ||||      |||
Db       1376 ATTTTTTTATATAATTTTTTTTTTAAATTTTAAATATATTTTATTAAAAAATAAAATTTT 1435

Qy       1197 TCTTAACAAAAAAAAAAAAAAA 1218
                ||||    ||||  |||| |
Db       1436 ATTTAATGTTAAAATTAAAATA 1457
```

RESULT 9
ADE84162
ID ADE84162 standard; DNA; 1501 BP.
XX
AC ADE84162;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human lymphoid cell proliferative disorder gene derived DNA #98.
XX
KW ds; lymphoid cell proliferative disorder; methylation;
KW methylated CpG dinucleotide; single nucleotide polymorphism; SNP;
KW diffuse large B-cell lymphoma; mantle cell lymphoma;
KW chronic lymphocytic leukemia; small lymphocytic lymphoma;
KW follicular lymphoma; diagnosis; prognosis.
XX
OS Homo sapiens.
XX
PN WO2003044226-A2.
XX
PD 30-MAY-2003.
XX
PF 25-NOV-2002; 2002WO-EP013265.
XX
PR 23-NOV-2001; 2001DE-01057491.
PR 28-DEC-2001; 2001DE-01064501.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimmrich I;
XX
DR WPI; 2003-457621/43.
XX
PT Detecting and differentiating between lymphoid cell proliferative
PT disorders comprises contacting a target nucleic acid with at least one
PT reagent that distinguishes between methylated and non-methylated CpG
PT dinucleotides.
XX
PS Claim 26; SEQ ID NO 158; 448pp; English.
XX
CC The invention relates to a method of detecting and differentiating
CC between lymphoid cell proliferative disorders associated with at least
CC one gene and/or their regulatory regions in a subject by contacting a
CC target nucleic acid in a biological sample obtained from the subject with
CC at least one reagent or series of reagents that distinguish between
CC methylated and non-methylated CpG dinucleotides within the target nucleic
CC acid. The genes and/or their regulatory regions are preferably selected
CC from MDR1, CSNK2B, EGR4, AR, CDK4, RB2, CDC25A, GPIb beta, MYOD1, CDH3,
CC MYCL1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2a, CDKN2B, FOS,
CC GSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RBL2, TGFBR2, TP73, CDKNIC,
CC GSK3beta, ESR1, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic
CC acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences
CC of the genes are useful for detecting the methylation state of all the
CC CpG dinucleotides within one or more the sequences, or their complements,
CC for determining the cytosine methylation state and or single nucleotide
CC polymorphisms (SNPs), and for differentiating at least two of the medical
CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,
CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular
CC lymphoma. They are also useful for detecting of a predisposition to,
CC differentiation between subclasses, diagnosis, prognosis, treating and/or
CC monitoring of lymphoid cell proliferative disorder. This sequence
CC represents a nucleic acid of a pretreated genomic DNA derived from the
CC above mentioned genes.
XX
SQ Sequence 1501 BP; 604 A; 0 C; 130 G; 767 T; 0 U; 0 Other;

Query Match 4.4%; Score 53.2; DB 10; Length 1501;
Best Local Similarity 46.1%; Pred. No. 0.52;
Matches 259; Conservative 0; Mismatches 293; Indels 10; Gaps 2;

```
Qy        663 TTCTTATTTTTAAAGTGGAAATTAGACTCCATCTTAGCTTCTTATTATGAATTTGAAGGA 722
              ||  |  |||| || |  |||||  | |  || ||    | |  |||   |||||  |
Db        900 TTAATGATTTTTAATTTTAAATTTAAATTAATTTTGATGTTTGTTTAATTATTTGTTGAT 959

Qy        723 ATCTTCCTTGCCTTGCACTGGGTATTATTATTCAACTAAAACTTCTATATCGTAATTCTT 782
               | ||  ||   ||  |     ||   |||   ||      |  |  | ||  | |   ||
Db        960 TTGTTTTTTAAATTTAATAATTTAAATTTAAATAATATTGAAATGAAAATTTTGAAATTT 1019

Qy        783 TCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTGGAAATCATGAAAATGAA 842
                  |  | ||    ||| || | |  |  | || ||     | |  || ||||   |
Db       1020 AAAATTTGAAATGTAATTTTTTTAAATTTTAATTTTATT----TATAAAATAAAAAAATA 1075

Qy        843 ATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCAAATAGCTGCAAGCAGA 902
              || | |||       |  ||    ||    | ||||  || |  ||| |  |  ||  | |
Db       1076 ATAATATTTATTTTATAAAATTATTATAAAATTTTAAAAAAATAAAAATATTTAAAAAAA 1135

Qy        903 AACTACGCTTTCCACGACATATTCTCTCTACTT------ATTATGGGTGGTATGTAATAT 956
              || |    |||  |  | | | |   |    ||      ||| | | |    |   |||
Db       1136 AAATTTAATTTAAATAAAAAAATAAATGATGTTAATTTAATTTTTGTTTTAAAAAAATGA 1195

Qy        957 TAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAGCTCGTGTC 1016
              || |   |  |  | |||||   | ||     ||  |  | |||    | |  |  | |
Db       1196 TATAAAAATAAAAAATTTTTTTTAAAATAAAATTAATTAAAATTTGTTATATTTTTTTTT 1255

Qy       1017 ATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTTTGAA 1076
              ||  |   | ||  |||| | || |   |   ||| |   |  ||     |||||   ||
Db       1256 ATTTTATATAAAATATTATAAAAATTATATAATAAAAAATAAAAATTTAATATTTAAAAA 1315

Qy       1077 AAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTAGTAATACTA 1136
              | ||   |   || ||      |||||||  ||| |    ||   |||  |  |  | ||
Db       1316 ATATTATAAAATTAAATTATTTTAAATTTTATTTTATATTATTAATTAAAATAATAAATA 1375

Qy       1137 ACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAAACAG 1196
              |   || ||   ||| | || |      ||||  |||   || ||||      |||
```

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Db       1376 ATTTTTTTATATAATTTTTTTTTTAAATTTTAAATATATTTTATTAAAAAATAAAATTTT 1435

Qy       1197 TCTTAACAAAAAAAAAAAAAAA 1218
              ||||    ||||  |||| |
Db       1436 ATTTAATGTTAAAATTAAAATA 1457


RESULT 10
AAA02542/c
ID   AAA02542 standard; cDNA; 1199 BP.
XX
AC   AAA02542;
XX
DT   19-MAY-2000  (first entry)
XX
DE   Human colon cancer cell line polynucleotide sequence SEQ ID NO:2533.
XX
KW   Human; colon cancer; tumour; diagnosis; gene expression product; probe;
KW   detection; cancerous state; metastasis; identification; breast cancer;
KW   oestrogen receptor-positive breast cancer; therapy;
KW   oestrogen receptor-negative breast cancer; lung cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9958675-A2.
XX
PD   18-NOV-1999.
XX
PF   13-MAY-1999;   99WO-US010602.
XX
PR   14-MAY-1998;   98US-0085426P.
PR   15-MAY-1998;   98US-0085537P.
PR   15-MAY-1998;   98US-0085696P.
PR   21-OCT-1998;   98US-0105234P.
PR   27-OCT-1998;   98US-0105877P.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Williams LT,  Escobedo J,  Innis MA,  Garcia PD,  Sudduth-Klinger J;
PI   Reinhard C,  Giese K,  Randazzo F,  Kennedy GC,  Pot D,  Kassam A;
PI   Lamson G,  Drmanac R,  Crkvenjakov R,  Dickson M,  Drmanac S,  Labat I;
PI   Leshkowitz D,  Kita D,  Garcia V,  Jones LW,  Stache-Crain B;
XX
DR   WPI; 2000-126369/11.
XX
PT   Polynucleotide library used to determine cancerous states of mammalian
PT   cells.
XX
PS   Claim 1; Page 1023-1024; 1097pp; English.
XX
CC   AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
CC   libraries constructed from human colon cancer cell lines. The present
CC   invention also describes a method of detecting differentially expressed
CC   genes correlated with a cancerous state of a mammalian cell, comprising
CC   detecting at least one differentially expressed gene product in a test
CC   sample derived from a cell suspected of being cancerous, where detection
CC   of the differentially expressed gene product is correlated with a
CC   cancerous state of the cell from which the test sample was derived. The
CC   polynucleotides sequences can be used in a method for detecting
CC   differentially expressed genes correlated with a cancerous state of a
CC   mammalian cell. The polynucleotides can also be used as probes for
CC   detecting and mapping related genes. They can be used in diagnosis and
CC   prognosis of diseases and disorders (e.g. identification of pre-
CC   metastatic or metastatic cancerous states, stages of cancer, or
CC   responsiveness of cancer to therapy). This is particularly for breast
CC   cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
CC   negative breast cancer, lung cancer, and colon cancer
XX
SQ   Sequence 1199 BP; 430 A; 98 C; 63 G; 370 T; 0 U; 238 Other;

  Query Match             4.3%;  Score 52.6;  DB 3;  Length 1199;
  Best Local Similarity   37.7%;  Pred. No. 0.67;

  Matches  268;  Conservative    0;  Mismatches  437;  Indels    6;  Gaps    3;

Qy        486 TCTATGAACCACAATCGTAACCCTATATTAAGAAAATTCGCTTTAGTCTACGCTCCTCTT 545
              | |||      | |      |      || |    | |||      |  |  |    | ||
Db       1180 TNTATANNNTAGAGANANANTTANTNATAATATATATTTNNNNAAATNNAGNATAATGTT 1121

Qy        546 TGTGGTGGTTTCTCTAATAAATGGTGGGGTAGGAAGCACAATCAACATCATATGTTCACA 605
              | |  | || |      |  | || ||   |||  ||    ||  | || || |    | |
Db       1120 TATAATTGTATNNAATAGTATTGATGAANTAGATAGATANATTNATAT-ATGTNAANANA 1062

Qy        606 AACAACATTCTAAAGGACGAAGATATCTAACACGATTACAAATTGTGGTAATTCCCCTTC 665
               |  | ||   |||     |||||  | ||     ||       || |  |         |
Db       1061 NATTATATATGAAANANGTAAGATNTATATATACATATNTNNTTATNTTNTAATNNAATA 1002

Qy        666 TTATTTTTAAAGTGGAAATTAGACTCCATCTTAGCTTCTTATTATGAATTTGAAGGAATC 725
              | | |         |   |  || |          |||| | | |||  ||    || ||
Db       1001 TNANTNNGTTCNTATNATCTATATATANNAANAGCTTATNAATATATATANTNAGTAANA 942

Qy        726 TTCCTTGCCTTGCACTGGGTATTATTATTCAACTAAAACTTCTATATCGTAATTCTTTCT 785
              ||   |  ||    |  | | ||||   |   |    |         ||| |   | |
Db        941 TTAAATTTATT-ATNTANNTNTATTTATANTAGATATNTATTATNTNAATAANTNNATAT 883

Qy        786 GAATTGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTGGAAATCATGAAAATGAAATG 845
               | || |     | | |    ||     |     ||  |  | |   |||| |  ||
Db        882 NATTTTAANNTAGTTATNNGTAGANNATANTATAAGTTTANATNTAAATTAAATNANNTG 823

Qy        846 AAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCAAATAGCTGCAAGCAGAAAC 905
               | |   | ||      |  | | ||          || ||  |  |  |    |   |
Db        822 TNAATAATANGATTTNATANNTNTCTATGAAAANTNNATGAATGATNTAAATAAATGTAG 763

Qy        906 TACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGGTATGTAATATTAGACTGAA 965
              | |  ||   |    |||||   | ||  ||||    |   || ||| |  |      |
Db        762 TTCTATTANTAGTNGATATTTNTTTTAANTATTTNTNGATATAAGTANTTNTNCNTATAT 703

Qy        966 CATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAGCTCGTGTCATAATTGCT 1025
                  |   ||| ||   ||| |      ||   | |  |  |    |||||
Db        702 TTNTNNANAATNTNATANATNNTTTTATNNTNGATAANTATATATTATAAATTAATTNNN 643

Qy       1026 GA----AGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTTTGAAAAATC 1081
               |    |  || ||  || |     | |   |   |     |  | |  ||    |
Db        642 TATNTNATTATNAATCAAATNTTNTNTGTATTATNTNGNTATNAAANTATANGAGNTNTG 583

Qy       1082 TCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTAGTAATACTAACAAT 1141
              |    ||      || |||||   | | ||  |   |||| |   |    ||    |  ||
Db        582 TTTNTTTAAGTTATTAATAATNATNTATTGTAANGATATNTATATTANNATTTNNANNAT 523

Qy       1142 TGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAA 1192
                | |  |  |||     |   || | |||     ||  | | | | |
Db        522 GANTANATANTTTATATNTAGTAAGTAATAATTTTCGATTNTTNTNATATA 472


RESULT 11
ABA92787_0
WP Sequence split into 7 fragments  LOCUS ABA92787 Accession Aba92787
WP     Fragment Name      Begin     End
WP     ABA92787_0             1    110000
WP     ABA92787_1        100001    210000
WP     ABA92787_2        200001    310000
WP     ABA92787_3        300001    410000
WP     ABA92787_4        400001    510000
WP     ABA92787_5        500001    610000
WP     ABA92787_6        600001    640681
ID   ABA92787 standard; DNA; 640681 BP.
XX
AC   ABA92787;
XX
DT   27-MAR-2002  (first entry)
XX
DE   Buchnera sp. genomic DNA SEQ ID NO:1.
XX
KW   Buchnera; cockroach-symbiotic bacterium; cockroach extermination;
KW   circular; ds.
XX
```

OS Buchnera sp.
XX
PN JP2001292771-A.
XX
PD 23-OCT-2001.
XX
PF 07-APR-2000; 2000JP-00107160.
XX
PR 07-APR-2000; 2000JP-00107160.
XX
PA (RIKA ) RIKAGAKU KENKYUSHO.
XX
DR WPI; 2002-126043/17.
XX
PT A genomic DNA of cockroach-symbiotic bacterium.
XX
PS Claim 1; Page 16-230; 237pp; Japanese.
XX
CC The present invention describes a gene (I) derived from Buchnera sp.
CC containing the DNA (a) or (b), (a) has a fully defined base pair sequence
CC selected from a table of sequences found in the Buchnera sp. genomic DNA
CC of ABA92787 given in the specification or is a DNA selected from
CC complementary DNA sequences, and (b) is a DNA which hybridises with the
CC DNA (a) and encodes a protein. Also described are: (1) a recombinant
CC vector (II) containing (I); (2) a transformant (III) containing (II); (3)
CC a genomic DNA of Buchnera sp. containing the sequence given in ABA92787;
CC (4) a plasmid derived from Buchnera sp. containing DNA (c) or (d), (c) is
CC a DNA containing a fully defined sequence given in ABA92788 or ABB92789
CC and (d) is a plasmid which hybridises with a DNA; and (5) a method for
CC the preparation of a protein in which (III) is cultured and the
CC expression protein of the objective protein is collected from the
CC resultant culture. The DNA is useful for developing agricultural
CC chemicals for exterminating cockroaches. The present sequence represents
CC the specifically claimed Buchnera sp. genomic DNA sequence, from the
CC present invention
XX
SQ Sequence 640681 BP; 237522 A; 83822 C; 84757 G; 234580 T; 0 U; 0 Other;

Query Match 4.3%; Score 52; DB 6; Length 110000;
Best Local Similarity 54.8%; Pred. No. 1.4;
Matches 103; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 1031 ATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTTTGAAAAATCTCACCTTTG 1090
Db 95585 AGTAAAAAAAATATTAATATACTATCAATAATTGAAATATTTTTTAAAAATCTTTTTCTAT 95644

Qy 1091 AAAATAAATAAATTTATTTTAAATGCATATTTTATTAGTAATACTAACAATTGTAGGAAA 1150
Db 95645 TTAAAAAACATATTTTTTATATATCTGACTAGTATTTTTTAAAAAAATCATTTTAATATT 95704

Qy 1151 TGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAAACAGTCTTAACAAAAAAA 1210
Db 95705 TTTTTGATATTAAAATGATTTTTTATTCTTAATATATATTATTCAGTTTATATAAAATAA 95764

Qy 1211 AAAAAAAA 1218
Db 95765 AAAATATA 95772

RESULT 12
ABX46053/c
ID ABX46053 standard; cDNA; 424 BP.
XX
AC ABX46053;
XX
DT 21-FEB-2003 (first entry)
XX
DE Bovine EST associated with lactation/muscle/fat deposition #11218.
XX
KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX

OS Bos Taurus.
XX
PN US2002137139-A1.
XX
PD 26-SEP-2002.
XX
PF 24-SEP-2001; 2001US-00960352.
XX
PR 12-JAN-1999; 99US-0115707P.
PR 11-JAN-2000; 2000US-00480902.
XX
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX
PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX
DR WPI; 2003-110599/10.
XX
PT New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
PT cattle breeding, or for genetically improving cattle.
XX
PS Claim 2; SEQ ID NO 11218; 245pp; English.
XX
CC The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non- translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX
SQ Sequence 424 BP; 228 A; 7 C; 32 G; 157 T; 0 U; 0 Other;

Query Match 4.2%; Score 51.8; DB 8; Length 424;
Best Local Similarity 63.0%; Pred. No. 0.85;
Matches 80; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 1093 AATAAATAAATTTATTTTAAATGCATATTTTATTAGTAATACTAACAATTGTAGGAAATG 1152
Db 194 AAAATTTTAATTTATTTTATTTTTAAATTTTTTTTATTTTTTTTATTTTTTTTTTTTTTT 135

Qy 1153 TGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAAACAGTCTTAACAAAAAAAAA 1212
Db 134 TATTTTTTTTTTTTTTATTTTTTTATTTTTAATTTAAAAAAAAAAAAAAAAAAAAAAAAA 75

Qy 1213 AAAAAAA 1219
Db 74 AAAAAAA 68

RESULT 13

```
ABL34044/c
ID   ABL34044 standard; DNA; 7319 BP.
XX
AC   ABL34044;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human immune system associated gene SEQ ID NO: 2017.
XX
KW   Human; immune system disease; cytosine methylation; antiasthmatic;
KW   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW   neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW   antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW   antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW   acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW   neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO200200928-A2.
XX
PD   03-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-EP007537.
XX
PR   30-JUN-2000; 2000DE-01032529.
PR   01-SEP-2000; 2000DE-01043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-130909/17.
XX
PT   Nucleic acid comprising fragment of chemically modified gene, useful for
PT   diagnosis and treatment of diseases associated with abnormal cytosine
PT   methylation.
XX
PS   Claim 1; SEQ ID NO 2017; 32pp + Sequence Listing; German.
XX
CC   The present invention provides a number of human immune system associated
CC   genes which are modified by the methylation of cytosines. The sequences
CC   can be used in the diagnosis and treatment of immune system disorders,
CC   including eye diseases such as retinopathy, neovascular glaucoma and
CC   macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC   leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC   rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC   diseases. The present sequence is a gene of the invention
XX
SQ   Sequence 7319 BP; 2188 A; 263 C; 1633 G; 3235 T; 0 U; 0 Other;

  Query Match             4.2%;  Score 51.8;  DB 6;  Length 7319;
  Best Local Similarity   48.7%;  Pred. No. 1.2;
  Matches  170;  Conservative    0;  Mismatches  177;  Indels    2;  Gaps    1;

Qy          3 TAAGCAAACTAAATTTAAAAAACAAGCATTATGGGAGTTGATAAGACTTAAGAAGAAATT 62
              ||| | |  |||||  | | || || ||||       || | || ||  ||  | ||| |
Db       1875 TAAACCACTTAAATCCATATAAAAATCATTTAAAATTTTAACAAAACACAAACAAAAAAT 1816

Qy         63 GTTCTTGAAAATAAACCCGAACTTCTCAACGAATACAAATTTATTTACAAGGATACTGAA 122
              |||| |||||| || | | ||  | | |    | ||    || || ||  ||||  ||
Db       1815 TATCTTTAAAATATACACAACCTAATAATCATTAAAAACAAAATCTAAAACTATACACAA 1756

Qy        123 TATGACTGCACTGAATATGCTAAATCAAA--TAAGCATCCTGGCGGTCTTAATTTCCTCA 180
              ||      | |  | |     ||| || |  ||| ||||       |   ||||||  |
Db       1755 TAATTACCCCCAAATTTAATAAAACCATAATTAACCATCAATTATTTAAAAATTTCACCG 1696

Qy        181 ATTTGTTTATTGATGAGAAGTAAGATTTGACTGAATATTTCAGAACACTCCATTCTAAGT 240
              |  || |||  | | ||  |    |  | |  | | |  | | |||  || |  || |
Db       1695 CATAATTCATTTCTAAAAAAAATATATAAATTATAAAATCAATATCACAACAATAAAATT 1636

Qy        241 AGGCTTTGAAAATTTTAAAATCCTTCCCTAAGACTGGCGCAAAATAAGAGGAGACTGAAT 300
                    ||||    |  |  ||||  | |||    ||||        | |   | |
Db       1635 TAAAAAATAAAAAAAAATCCTTAATCCCACAAACTAATACAAATATCTTTTAAATATATT 1576

Qy        301 CTTCAAAGAGATTCTCAATATTAAAGAAAAAGCTTAAGCATTTATTCGA 349
              |   | | | | | |  | | |||| || ||    ||    | |||| |
Db       1575 CACTATATATAATTTTACAATAAAAAACAAAAAAAACTTATAATTCTA 1527


RESULT 14
ABL32101/c
ID   ABL32101 standard; DNA; 5728 BP.
XX
AC   ABL32101;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human immune system associated gene SEQ ID NO: 74.
XX
KW   Human; immune system disease; cytosine methylation; antiasthmatic;
KW   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW   neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW   antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW   antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW   acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW   neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO200200928-A2.
XX
PD   03-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-EP007537.
XX
PR   30-JUN-2000; 2000DE-01032529.
PR   01-SEP-2000; 2000DE-01043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-130909/17.
XX
PT   Nucleic acid comprising fragment of chemically modified gene, useful for
PT   diagnosis and treatment of diseases associated with abnormal cytosine
PT   methylation.
XX
PS   Claim 1; SEQ ID NO 74; 32pp + Sequence Listing; German.
XX
CC   The present invention provides a number of human immune system associated
CC   genes which are modified by the methylation of cytosines. The sequences
CC   can be used in the diagnosis and treatment of immune system disorders,
CC   including eye diseases such as retinopathy, neovascular glaucoma and
CC   macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC   leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC   rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC   diseases. The present sequence is a gene of the invention
XX
SQ   Sequence 5728 BP; 1931 A; 49 C; 885 G; 2863 T; 0 U; 0 Other;

  Query Match             4.2%;  Score 51.4;  DB 6;  Length 5728;
  Best Local Similarity   54.7%;  Pred. No. 1.4;
  Matches  123;  Conservative    0;  Mismatches  101;  Indels    1;  Gaps    1;

Qy        989 TTTCTACAGATTACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCT 1048
              | |  ||  |  | | |||   | | ||| ||      || ||  ||| ||        |
Db       2910 TCTAAACGAAAAAACGAAACTCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAATTCTTT 2851

Qy       1049 TAAGATTCATGAAGGACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATT 1108
              |||  ||||| ||      | ||      ||| |||  | || || ||||| ||||  |||
Db       2850 TAAATTTCATCAATTTTATTTTAAAACTAAAACTCTTCATTAAATATAAAAAAATCAATT 2791
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Qy       1109 TTAAATGCATATTTTATTAGTA-ATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTT 1167
Db       2790 CAAAATTTCTATTCAATCATAATAAATTTAAAATTTTTTTAAATTTCTTTATATTTAACA 2731

Qy       1168 ACTTATTACTTTTTAATCTGAGAAAACAGTCTTAACAAAAAAAAA 1212
Db       2730 ATATATTACATTATAATATTATAATAAAAACTAAATAAACTAATA 2686
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RESULT 15
AAS46709/c
ID AAS46709 standard; DNA; 5750 BP.
XX
AC AAS46709;
XX
DT 18-DEC-2001 (first entry)
XX
DE Tumour suppressor gene derived chemically modified sequence #432.
XX
KW Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
KW tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW cytosine methylation; ds.
XX
OS Homo sapiens.
XX
PN WO200168912-A2.
XX
PD 20-SEP-2001.
XX
PF 15-MAR-2001; 2001WO-EP002955.
XX
PR 15-MAR-2000; 2000DE-01013847.
PR 06-APR-2000; 2000DE-01019058.
PR 07-APR-2000; 2000DE-01019173.
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-602752/68.
XX
PT Fragments of chemically modified genes associated with tumor suppressor
PT genes and oncogenes, useful in designing primers and probes for analyzing
PT diseases associated with cytosine methylation state e.g. cancer.
XX
PS Claim 1; SEQ ID NO 432; 27pp; English.
XX
CC The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and oncogenes
CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and
CC 500 are missing from the sequence listing) sequences (Ss) and sequences
CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid-
CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of
CC probes for detecting the cytosine methylation state and/or single
CC nucleotide polymorphisms and also to be used in an array for analysing
CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The
CC probes can also be used in a method for ascertaining genetic and/or
CC epigenetic parameters for the diagnosis and/or therapy of existing
CC diseases or the predisposition to specific diseases, by analysing
CC cytosine methylations. The parameters may be compared to another set of
CC genetic and/or epigenetic parameters, the differences serving as basis
CC for diagnosis and/or prognosis events which are disadvantageous to
CC patients. The present sequence is one of the 533 genomic sequences
CC derived from tumour suppressor genes and oncogenes. Sequences with even
CC numbered Seq ID numbers are the complementary sequence of the
CC corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID
CC 535, except for those whose partner sequence is missing). Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 5750 BP; 1736 A; 103 C; 1392 G; 2519 T; 0 U; 0 Other;

Query Match 4.2%; Score 51.2; DB 4; Length 5750;
Best Local Similarity 45.7%; Pred. No. 1.5;
Matches 179; Conservative 0; Mismatches 213; Indels 0; Gaps 0;

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Db       4820 AAATATTTAAAATAAAAATAACGACACTAAATCTTAAAAAAATAAATCTTTCAAACAAAA 4761

Qy        887 AATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGG 946
Db       4760 AACAAATATAAACAATAAATATCCCACGAAAAAAATTCCCTCTAAAATACGCCCTAAAAA 4701

Qy        947 TATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAA 1006
Db       4700 AACGAAAAAATATTTTATAAAAAACTTATTTTAAAAACTTTCTCTTTCTAAATATCTCCT 4641

Qy       1007 AGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACC 1066
Db       4640 TTATCCTATTTAAAATTATTAAACCTTCATACTATTTAACCTCAAAATATTTAACTACTT 4581

Qy       1067 TATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATT 1126
Db       4580 AAAATATTCAAAATTAAACCTATAATCAATCAAAATAAAATAAAATCTATTTCTTAATTT 4521

Qy       1127 AGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCT 1186
Db       4520 ATTTATTTATTTATTTTTTTTTTATTTTATTTATTTATTTATTTTTTTTAAAATAAAATCT 4461

Qy       1187 GAGAAAACAGTCTTAACAAAAAAAAAAAAAAA 1218
Db       4460 CGCCCTATCGCCCAAACTAAAATACAATAACA 4429
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Search completed: January 19, 2005, 14:11:06
Job time : 685 secs

GenCore version 5.1.6


OM nucleic - nucleic search, using sw model

Run on: January 18, 2005, 21:56:08 ; Search time 5526 Seconds
(without alignments)
10431.803 Million cell updates/sec

Title: US-10-070-666A-1
Perfect score: 1219
Sequence: 1 agtaagcaaactaaatttaa.....taacaaaaaaaaaaaaaaaa 1219

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
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13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| 1 | | 1219 | 100.0 | 1219 | 6 | AX098429 | AX098429 Sequence |
| 2 | | 614.4 | 50.4 | 2492 | 6 | AX098431 | AX098431 Sequence |
| 3 | c | 64.2 | 5.3 | 266544 | 3 | AC116956 | AC116956 Dictyoste |
| 4 | | 64 | 5.3 | 2000 | 6 | AX655393 | AX655393 Sequence |
| 5 | c | 62.4 | 5.1 | 252632 | 3 | AE014818 | AE014818 Plasmodiu |
| 6 | | 59 | 4.8 | 8056 | 6 | AX599046 | AX599046 Sequence |
| 7 | | 58.4 | 4.8 | 1141 | 6 | AX083744 | AX083744 Sequence |
| 8 | c | 58 | 4.8 | 6103 | 6 | AX346592 | AX346592 Sequence |
| 9 | | 58 | 4.8 | 253001 | 3 | AE014834 | AE014834 Plasmodiu |
| 10 | c | 57.8 | 4.7 | 3026 | 3 | AF324424 | AF324424 Ichthyoph |
| 11 | c | 57.4 | 4.7 | 8056 | 6 | AX598900 | AX598900 Sequence |
| 12 | c | 57 | 4.7 | 331039 | 3 | AC116979 | AC116979 Dictyoste |
| 13 | c | 56.8 | 4.7 | 7079 | 3 | AF362375 | AF362375 Dictyoste |
| 14 | | 56.8 | 4.7 | 159835 | 2 | CR387984 | CR387984 Danio rer |
| 15 | c | 56.4 | 4.6 | 76568 | 3 | MBREV | AF538053 Monosiga |
| 16 | | 56.2 | 4.6 | 111882 | 3 | AC115612 | AC115612 Dictyoste |
| 17 | c | 55.6 | 4.6 | 88549 | 3 | AC116924 | AC116924 Dictyoste |
| 18 | | 55.4 | 4.5 | 110000 | 2 | PFMAL13_14 | Continuation (15 o |
| 19 | | 55.2 | 4.5 | 250029 | 3 | AE014838 | AE014838 Plasmodiu |
| 20 | | 55.2 | 4.5 | 250053 | 3 | AE014825 | AE014825 Plasmodiu |
| 21 | c | 54.8 | 4.5 | 3606 | 3 | DDI1093A | M19469 Dictyosteli |
| 22 | | 54.8 | 4.5 | 125623 | 3 | AC115599 | AC115599 Dictyoste |
| 23 | | 54.8 | 4.5 | 229947 | 2 | CR394564 | CR394564 Danio rer |
| 24 | c | 54.6 | 4.5 | 8056 | 6 | AX599046 | AX599046 Sequence |
| 25 | c | 54.6 | 4.5 | 110000 | 1 | AP006628_6 | Continuation (7 of |
| 26 | c | 54.4 | 4.5 | 1141 | 6 | AX083744 | AX083744 Sequence |
| 27 | c | 54.4 | 4.5 | 134768 | 5 | BX537293 | BX537293 Zebrafish |
| 28 | | 54.2 | 4.4 | 348174 | 3 | CR382399 | CR382399 Plasmodiu |
| 29 | | 54 | 4.4 | 183285 | 2 | BX899180 | BX899180 Danio rer |
| 30 | | 54 | 4.4 | 281723 | 3 | PFA929359 | AL929359 Plasmodiu |
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| 32 | c | 53.4 | 4.4 | 197225 | 9 | AC093835 | AC093835 Homo sapi |
| 33 | c | 53.4 | 4.4 | 341050 | 3 | PFA929357 | AL929357 Plasmodiu |
| 34 | | 53.2 | 4.4 | 1501 | 6 | AX598988 | AX598988 Sequence |
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| 36 | c | 53.2 | 4.4 | 6099 | 3 | AF482382 | AF482382 Dictyoste |
| 37 | c | 53.2 | 4.4 | 180915 | 8 | GTAJ10592 | AJ010592 Guillardi |
| 38 | | 53.2 | 4.4 | 190015 | 2 | AC140056 | AC140056 Rattus no |
| 39 | | 53 | 4.3 | 1192 | 9 | HSA323759 | AJ323759 Homo sapi |
| 40 | | 53 | 4.3 | 104992 | 2 | AC005504 | AC005504 Plasmodiu |
| 41 | | 53 | 4.3 | 169546 | 2 | AC004157 | AC004157 Plasmodiu |
| 42 | c | 53 | 4.3 | 250421 | 3 | AE014849 | AE014849 Plasmodiu |
| 43 | | 52.8 | 4.3 | 156060 | 2 | AC004153 | AC004153 Plasmodiu |
| 44 | | 52.8 | 4.3 | 250707 | 3 | AE014848 | AE014848 Plasmodiu |
| 45 | c | 52.6 | 4.3 | 1199 | 6 | BD221420 | BD221420 Human gen |

ALIGNMENTS

RESULT 1
AX098429
LOCUS AX098429 1219 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 1 from Patent WO0120000.
ACCESSION AX098429
VERSION AX098429.1 GI:13537718
KEYWORDS .
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1
AUTHORS Ruesing,M., Kiy,T. and Dominitzki,A.
TITLE Nucleic acid which is obtained from tetrahymena and which codes for a delta-6-desaturase, the production thereof and use
JOURNAL Patent: WO 0120000-A 1 22-MAR-2001;
Axiva GmbH (DE)
FEATURES Location/Qualifiers
source 1. .1219
/organism="Tetrahymena thermophila"
/mol_type="unassigned DNA"
/db_xref="taxon:5911"
ORIGIN

Query Match 100.0%; Score 1219; DB 6; Length 1219;
Best Local Similarity 100.0%; Pred. No. 4.2e-202;
Matches 1219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGTAAGCAAACTAAATTTAAAAAACAAGCATTATGGGAGTTGATAAGACTTAAGAAGAAA 60
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Db          1 AGTAAGCAAACTAAATTTAAAAAACAAGCATTATGGGAGTTGATAAGACTTAAGAAGAAA 60

Qy         61 TTGTTCTTGAAAATAAACCCGAACTTCTCAACGAATACAAATTTATTTACAAGGATACTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGTTCTTGAAAATAAACCCGAACTTCTCAACGAATACAAATTTATTTACAAGGATACTG 120

Qy        121 AATATGACTGCACTGAATATGCTAAATCAAATAAGCATCCTGGCGGTCTTAATTTCCTCA 180
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Db        121 AATATGACTGCACTGAATATGCTAAATCAAATAAGCATCCTGGCGGTCTTAATTTCCTCA 180

Qy        181 ATTTGTTTATTGATGAGAAGTAAGATTTGACTGAATATTTCAGAACACTCCATTCTAAGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        181 ATTTGTTTATTGATGAGAAGTAAGATTTGACTGAATATTTCAGAACACTCCATTCTAAGT 240

Qy        241 AGGCTTTGAAAATTTTAAAATCCTTCCCTAAGACTGGCGCAAAATAAGAGGAGACTGAAT 300
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Db        241 AGGCTTTGAAAATTTTAAAATCCTTCCCTAAGACTGGCGCAAAATAAGAGGAGACTGAAT 300

Qy        301 CTTCAAAGAGATTCTCAATATTAAAGAAAAAGCTTAAGCATTTATTCGAACCAAACTGGC 360
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Db        301 CTTCAAAGAGATTCTCAATATTAAAGAAAAAGCTTAAGCATTTATTCGAACCAAACTGGC 360

Qy        361 CTATCGAAATTGGTTTATTCTTAACTACCTTTACTTTATTTGTCACTGGATGTTTGACTC 420
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Db        361 CTATCGAAATTGGTTTATTCTTAACTACCTTTACTTTATTTGTCACTGGATGTTTGACTC 420

Qy        421 AAAAGTGGTATTTCTCTATTCCCCTTCTTGTCTTAATGCAAATCATCAGTGGTTGGATTG 480
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Qy        481 GTCACTCTATGAACCACAATCGTAACCCTATATTAAGAAAATTCGCTTTAGTCTACGCTC 540
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Qy        541 CTCTTTGTGGTGGTTTCTCTAATAAATGGTGGGGTAGGAAGCACAATCAACATCATATGT 600
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Qy        601 TCACAAACAACATTCTAAAGGACGAAGATATCTAACACGATTACAAATTGTGGTAATTCC 660
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Qy        661 CCTTCTTATTTTTAAAGTGGAAATTAGACTCCATCTTAGCTTCTTATTATGAATTTGAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCTTCTTATTTTTAAAGTGGAAATTAGACTCCATCTTAGCTTCTTATTATGAATTTGAAG 720

Qy        721 GAATCTTCCTTGCCTTGCACTGGGTATTATTATTCAACTAAAACTTCTATATCGTAATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAATCTTCCTTGCCTTGCACTGGGTATTATTATTCAACTAAAACTTCTATATCGTAATTC 780

Qy        781 TTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTGGAAATCATGAAAATG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTGGAAATCATGAAAATG 840

Qy        841 AAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCAAATAGCTGCAAGCA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCAAATAGCTGCAAGCA 900

Qy        901 GAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGGTATGTAATATTAGA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        961 CTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAGCTCGTGTCATAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAGCTCGTGTCATAA 1020

Qy       1021 TTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTTTGAAAAAT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1081 CTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTAGTAATACTAACAA 1140
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Qy       1141 TTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAAACAGTCTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAAACAGTCTT 1200

Qy       1201 AACAAAAAAAAAAAAAAAA 1219
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Db       1201 AACAAAAAAAAAAAAAAAA 1219
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RESULT 2
AX098431

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LOCUS       AX098431               2492 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 3 from Patent WO0120000.
ACCESSION   AX098431
VERSION     AX098431.1  GI:13537719
KEYWORDS    .
SOURCE      Tetrahymena thermophila
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1
  AUTHORS   Ruesing,M., Kiy,T. and Dominitzki,A.
  TITLE     Nucleic acid which is obtained from tetrahymena and which codes for
            a delta-6-desaturase, the production thereof and use
  JOURNAL   Patent: WO 0120000-A 3 22-MAR-2001;
            Axiva GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .2492
                     /organism="Tetrahymena thermophila"
                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match           50.4%;  Score 614.4;  DB 6;  Length 2492;
  Best Local Similarity  99.8%;  Pred. No. 3.6e-97;
  Matches  615;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         589 AACATCATATGTTCACAAACAACATTCTAAAGGACGAAGATATCTAACACGATTACAAAT 648
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Qy         649 TGTGGTAATTCCCCTTCTTATTTTTAAAGTGGAAATTAGACTCCATCTTAGCTTCTTATT 708
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         709 ATGAATTTGAAGGAATCTTCCTTGCCTTGCACTGGGTATTATTATTCAACTAAAACTTCT 768
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1772 ATGAATTTGAAGGAATCTTCCTTGCCTTGCACTGGGTATTATTATTCAACTAAAACTTCT 1831

Qy         769 ATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTGGAA 828
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Db        1832 ATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTGGAA 1891

Qy         829 ATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGAACATCAAA 888
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         889 TAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTATGGGTGGTA 948
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Qy         949 TGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAG 1008
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Db        2012 TGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATTACCCAAAG 2071

Qy        1009 CTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTA 1068
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2072 CTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTA 2131

Qy        1069 TTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATATTTTATTAG 1128
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Qy        1129 TAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGA 1188
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2192 TAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGA 2251

Qy        1189 GAAAACAGTCTTAACA 1204
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Db        2252 GAAAACAGTCTTAACA 2267
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RESULT 3
AC116956/c

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LOCUS       AC116956              266544 bp    DNA     linear   INV 12-MAR-2003
DEFINITION  Dictyostelium discoideum chromosome 2 map 1418423-1684967 strain
            AX4, complete sequence.
ACCESSION   AC116956 AC116980 AC115678
VERSION     AC116956.2  GI:28828496
KEYWORDS    HTG.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 266544)
  AUTHORS   Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P.,
            Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K.,
            Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
            Noegel,A.A.
  TITLE     Sequence and analysis of chromosome 2 of Dictyostelium discoideum
  JOURNAL   Nature 418 (6893), 79-85 (2002)
  MEDLINE   22092622
   PUBMED   12097910
  REMARK    The Dictyostelium Genome Sequencing Consortium
REFERENCE   2  (bases 1 to 266544)
  AUTHORS   Baumgart,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-APR-2002) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenberstr. 11, Jena 07745, Germany
REFERENCE   3  (bases 1 to 266544)
  AUTHORS   Baumgart,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-MAR-2003) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenberstr. 11, Jena 07745, Germany
REFERENCE   4  (bases 1 to 266544)
  AUTHORS   Baumgart,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenberstr. 11, Jena 07745, Germany
COMMENT     On or before Mar 4, 2003 this sequence version replaced
            gi:20042935, gi:19682974, gi:19919988.
            CDS predictions from GeneID do not necessarily reflect true genes.
            Further Information is available from IMB Jena, Department of
            Genome Analysis
            (http://genome.imb-jena.de/dictyostelium/)
            and the Univerity Colonge, Institute for Biochemistry I
            (http://www.uni-koeln.de/dictyostelium/project.shtml
            Funding
            Agency : Deutsche Forschungsgemeinschaft (DFG).
FEATURES             Location/Qualifiers
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                     /db_xref="GI:28828559"
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                     SVKYDFETTNNSTFINGQYPVTVYMCNGECGTMYSTLLNQTTSYFTISNPTPTPTPTP
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                     clone:A130067E11 product:cyclin C, full insert sequence"
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  Matches  140;  Conservative    0;  Mismatches  108;  Indels    1;  Gaps    1;

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              |||||  |   |||||  || ||| |   || |  || ||| |    |   ||    || |
Db     248420 CTTTTAACTTCAAATTGTTTACTAGAATGTAACGTAATCTCATCAGAACTTTTGGAAATA 248361

Qy       1031 ATTAAAGAAGTGGAACCTTAAGATTCATGAAGGACCTATTTTTGAAAAATCTCACCTTTG 1090
              |||||  |   |  || ||||  ||| ||  |  |   ||  || | | || | |   |
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Qy       1091 AAAATAAATAAATTTATTTTAAATGCATATTTTATTAGTAATACTAACAATTGTAGGAAA 1150
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Qy       1151 TGTGTTATGGTTTGTTTACTTATTACTTTTTAATCTGAGAAAACAGTCTTAACAAAAAAA 1210
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Db     248240 TTTAA-ATGATTTATTTAATTCTTTATATTTTATTTATAAAAAAAAAAAAAACAAAAAAA 248182

Qy       1211 AAAAAAAAA 1219
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Db     248181 AAAAACAAA 248173


RESULT 4
AX655393
LOCUS       AX655393               2000 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 5263 from Patent WO03000898.
ACCESSION   AX655393
VERSION     AX655393.1  GI:29158207
KEYWORDS    .
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1
  AUTHORS   Chang,H.S., Chen,W., Cooper,B., Glazebrook,J., Goff,S.A., Hou,Y.M.,
            Katagiri,F., Quan,S., Tao,Y., Whitham,S., Xie,Z., Zhu,T. and Zou,G.
  TITLE     Plant genes involved in defense against pathogens
  JOURNAL   Patent: WO 03000898-A 5263 03-JAN-2003;
            Syngenta Participations AG (CH)
FEATURES             Location/Qualifiers
     source          1. .2000
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ORIGIN

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Qy        103 TTATTTACAAGGATACTGAATATGACTGCACTGAATATGCTAAATCAAATAAGCATCCTG 162
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Db        280 WSYKMWMCTAYKKSYYSRWCYMYRGGGWRGATRYWGRGYMSRMAMMYKKMYWYRGYKGMK 339

Qy        223 GAACACTCCATTCTAAGTAGGCTTTGAAAATTTTAAAATCCTTCCCTAAGACTGGCGCAA 282
              : : |  :::  : ::::|  :  ::::::|   ::| ::: |:  : :::| :: :: :
Db        340 RGWWAGRMMMRSMCRWSKACYYMRWRMWRMTRRRRWAKKSSRTSRRKKRKWCMRKRKYKR 399

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Db        460 MYRWRKKKCSRTTMWGKTRGGMMGTMGRCRYKKRSGMKRKCRRRRWGRMYRMRWKRYYMS 519

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Db        520 ARYTMRYCARKKYSYSAARKARCWYRGKGYYWAGMWMKRYKRMYMYKMMWWYKRKYSKCS 579

Qy        460 AAATCATCAGTGGTTGGATTGGTCACTCTATGAACCACAATCGTAACCCTATATTAAGAA 519
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Qy        520 AATTCGCTTTAGTCTACGCTCCTCTTTGTGGTGGTTTCTCTAATAAATGGTGGGGTAGGA 579
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Qy        580 AGCACAATCAACATC-----ATATGTTCACAAACAACATTCTAAAGGACGAAGATATCTA 634
               :::: :|::|  |:     :|  ::  :::     : : ::  :: :: :  ::|: :
Db        700 YRYRSYMTYMAWYTSSTRMAMTGMKYSGRYWTSWYKYCKCSWKYRSMWYYWSWWWAKTWK 759

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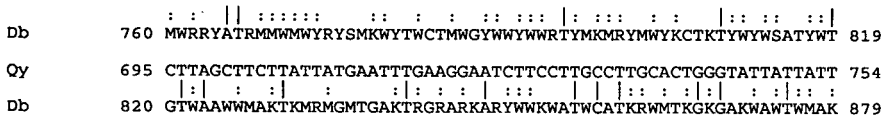

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Qy        755 CAACTAAAACTTCTATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTC 814

Db        880 AWRKYYWSWMRAWYYYYKTRRTRYKTCWWKARWGSWAYWRMWWKGSAKMWWMWKGGRWGW 939

Qy        815 TATTCTTGTTGGAAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATT 874

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RESULT 5
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LOCUS       AE014818              252632 bp    DNA     linear   INV 07-OCT-2002
DEFINITION  Plasmodium falciparum 3D7 chromosome 14 section 3 of 13 of the
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ACCESSION   AE014818 AE014187
VERSION     AE014818.1  GI:23497188
KEYWORDS    .
SOURCE      Plasmodium falciparum 3D7
  ORGANISM  Plasmodium falciparum 3D7
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 252632)
  AUTHORS   Gardner,M.J., Hall,N., Fung,E., White,O., Berriman,M., Hyman,R.W.,
            Carlton,J.M., Pain,A., Nelson,K.E., Bowman,S., Paulsen,I.T.,
            James,K., Eisen,J.A., Rutherford,K., Salzberg,S.L., Craig,A.,
            Kyes,S., Chan,M.-S., Nene,V., Shallom,S.J., Suh,B., Peterson,J.,
            Angiuoli,S., Pertea,M., Allen,J., Selengut,J., Haft,D.,
            Mather,M.W., Vaidya,A.B., Martin,D.M.A., Fairlamb,A.H.,
            Fraunholz,M.J., Roos,D.S., Ralph,S.A., McFadden,G.I.,
            Cummings,L.M., Subramanian,G.M., Mungall,C., Venter,J.C.,
            Carucci,D.J., Hoffman,S.L., Newbold,C., Davis,R.W., Fraser,C.M. and
            Barrell,B.
  TITLE     Genome sequence of the human malaria parasite Plasmodium falciparum
  JOURNAL   Nature 419 (6906), 498-511 (2002)
   PUBMED   12368864
REFERENCE   2  (bases 1 to 252632)
  AUTHORS   Gardner,M.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2002) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
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                     /rpt_type=tandem
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Best Local Similarity 47.7%; Pred. No. 0.11;
Matches 253; Conservative 0; Mismatches 266; Indels 11; Gaps 2;

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Db      70032 TTTCCTTTTTTTTTTTTTTTTAAATATTCTTTTGTATATTTCTCTAAATATATTTATAT 69973

Qy        756 AACTAAAACTTCTATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTT------CAGT 809
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Db      69972 ATATATATATTAATATATTTATATAATTATATAATTATATATGTATACTTCCTTTCCTTT 69913

Qy        810 GCTTCTATTCTTGTTGGAAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTA 869
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Db      69912 CCTTTTATTTTATTTTATATTTCTTAAAATTACATAAAATTTAAAAGATTGTTAATTTTT 69853

Qy        870 CCATTTTTCGAACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCT 929
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Qy        930 CTACTTATTATGGGTGGTATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCT 989
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Qy        990 TTCTACAGATTACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTT 1049
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Qy       1050 AAGATTCATGAAGGACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTT 1109
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Qy       1110 TAAATGCATATTTTATTAGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTAC 1169
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Qy       1170 TTATTACTTTTTAATCTGAGAAAACAGTCTTAACAAAAAAAAAAAAAAAA 1219
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RESULT 6
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LOCUS       AX599046                8056 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 386 from Patent WO02077272.
ACCESSION   AX599046
VERSION     AX599046.1  GI:28399186
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 386 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .8056
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                     /note="chemically treated genomic DNA (Homo sapiens)"
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Query Match 4.8%; Score 59; DB 6; Length 8056;

Best Local Similarity 44.3%; Pred. No. 0.83;
Matches 483; Conservative 0; Mismatches 585; Indels 23; Gaps 5;

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Qy        101 ATTTATTTACAAGGATACTGAATATGACTGCACTGAATATGCTAAATCAAATAAGCATCC 160
Db       2396 ATTTTTTGAAAATTAAAAAAAAAATAATTTATTTATTTTAAAAATTAATTTTTTTTTAT 2455

Qy        161 TGGCGGTCTTAATTTCCTCAATTTGTTTATTGATGAGAAGTAAGATTTGACTGAATATTT 220
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Qy        221 CAGA-----ACACTCCATTCTAAGTAGGCTTTGAAAATTTTAAAATCCTTCCCTAAGACT 275
Db       2516 AAAAAAAATAAATTAAATTATAAAATAAATTAAAAAATTTAAAAATTTAAATAAAATTTT 2575

Qy        276 GGCGCAAAATAAGAGGAGACTGAATCTTCAAAGAGATTCTCAATATTAAAGAAAAAGCTT 335
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Qy        336 AAGCATTTATTCGAACCAAACTGGCCTATCGAAATTGGTTTATTCTTAACTACCTTTACT 395
Db       2636 ATAAAAAAAAATGTTAAAATTTAAAATTTTAAAAATAATAAATTTTTAAATTTTTTTAAA 2695

Qy        396 TTATTTGTCACTGGATGTTTGACTCAAAAGTGGTATTTCTCTATTCCCCTTCTTGTCTTA 455
Db       2696 TTTATTATTTTTTTTTTTTAATAAAAATAATTTGTTAAATAAAT----------TATTA 2744

Qy        456 ATGCAAATCATCAGTGGTTGGATTGGTCACTCTATGAACCACAATCGTAACCCTATATTA 515
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Qy        516 AGAAAATTCGCTTTAGTCTACGCTCCTCTTTGTGGTGGTTTCTCTAATAAATGGTGGGGT 575
Db       2805 TTAAAATTGTTATTAATAATAAATGATATTTTTTTATAAAATATTAAAAATTTGAAATTA 2864

Qy        576 AGGAAGCACAATCAACATCATATGTTCACAAACAACATTCTAAAGGACGAAGATATCTAA 635
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Qy        696 TTAGCTTCTTATTATGAATTTGAAGGAATCTTCCTTGCCTT---GCACTGGGTATTATTA 752
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Qy        753 TTCAACTAAAACTTCTATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTTCAGTGCT 812
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Qy        813 TCTATTCTTGTTGGAAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCA 872
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Qy        873 TTTTTCGAACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTA 932
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Qy        933 CTTATTATGGGTGGTATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTC 992
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Qy        993 TACAGATTACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAG 1052
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Qy       1053 ATTCATGAAGGACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAA 1112
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Db       3461 TTATTAATAAA 3471
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RESULT 7
AX083744
LOCUS AX083744 1141 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 22 from Patent WO0111061.
ACCESSION AX083744
VERSION AX083744.1 GI:13185472
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Kunst,L. and Clemens,S.
TITLE Regulation of embryonic transcription in plants
JOURNAL Patent: WO 0111061-A 22 15-FEB-2001;
UNIVERSITY OF BRITISH COLUMBIA (CA)
FEATURES Location/Qualifiers
source 1. .1141
/organism="synthetic construct"
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promoter 1. .1141
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ORIGIN

Query Match 4.8%; Score 58.4; DB 6; Length 1141;
Best Local Similarity 11.9%; Pred. No. 1.6;
Matches 83; Conservative 261; Mismatches 352; Indels 4; Gaps 1;

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Qy        578 GAAGCACAATCAACATCATATGTTCACAAACAACATTCTAAAGGACGAAGATATCTAACA 637
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Qy        638 CGATTACAAATTGTGGTAATTCCCCTTCTTATTTTTAAAGTGGAAATTAGACTCCATCTT 697
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Qy        698 AGCTTCTTATTATGAATTTGAAGGAATCTTCCTTGCCTTGCACTGGGTATTATTATTCAA 757
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Qy        758 CTAAAACTTCTATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTAT 817
Db        369 VWHSAWKKWHANAAHYSRKKWTBYKRKTMVNNNNGTTMWKRMWAWYWKMDMDWBGTYNNN 428

Qy        818 TCTTGTTGGAAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTT 877
Db        429 NNGGRTYYGWTKNKKMWTYYKWKANNCKWRAWDHKTCTHNNTTWWKMKTYWNNCYWKSMT 488

Qy        878 CGAACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTAT 937
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Qy        998 ATTACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCA 1057
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Qy       1178 TTTTAATCTGAGAAAACAGTCTTAACAAAAAAAAAAAAAA 1217

Db        785 NNNTYRGVVTNTAARDGWANNNNNNNNNNNNNGWSDMWV 824


RESULT 8
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LOCUS       AX346592               6103 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 1663 from Patent WO0200928.
ACCESSION   AX346592
VERSION     AX346592.1  GI:18494478
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A., Piepenbrock,C. and Berlin,K.
  TITLE     Diagnosis of diseases associated with the immune system
  JOURNAL   Patent: WO 0200928-A 1663 03-JAN-2002;
            Epigenomics AG (DE)
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  Query Match             4.8%;  Score 58;  DB 6;  Length 6103;
  Best Local Similarity   46.6%;  Pred. No. 1.3;
  Matches  221;  Conservative    0;  Mismatches  250;  Indels    3;  Gaps    1;

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Qy        808 GTGCTTCTATTCTTGTTGGAAATCATGAAAATGAAAT---GAAATTCGAAAGAAGAATCA 864

Db       1784 AAACTACTAATTTTATCCAAAACAAAATTAACCAACTATAAAAATCAAAACCAAAAAAAA 1725

Qy        865 CTTTACCATTTTTCGAACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACATAT 924

Db       1724 ACAACTCCTTTTCAAATCACACAACAAATTAAAAACTAAACAAAAATTATAACTTAAATC 1665

Qy        925 TCTCTCTACTTATTATGGGTGGTATGTAATATTAGACTGAACATCACTTTTTCCCATAAA 984

Db       1664 TTTTACTACATCGTATAATAACTTATTACATATCATCTCCACCACACCCTCTTTAATAAA 1605

Qy        985 TTCCTTTCTACAGATTACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGA 1044

Db       1604 TCCCATAAAACAAAATACTCCAATCTCCAACTCATTAAAATACATAAAAAAAAAACAATA 1545

Qy       1045 ACCTTAAGATTCATGAAGGACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATT 1104

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Qy       1105 TATTTTAAATGCATATTTTATTAGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTG 1164

Db       1484 AATAATAAATACATCTATTATAAAAAATCCTACATAAAAAAAAAAATTAAATATACTAAA 1425

Qy       1165 TTTACTTATTACTTTTTAATCTGAGAAAACAGTCTTAACAAAAAAAAAAAAAAA 1218

Db       1424 TACGTTCATTTTTCTAATCAAAAATTAAAACATATTAAAAAATAAAAACAAAAA 1371


RESULT 9
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LOCUS       AE014834               253001 bp    DNA     linear   INV 07-OCT-2002
DEFINITION  Plasmodium falciparum 3D7 chromosome 10 section 6 of 7 of the
            complete sequence.
ACCESSION   AE014834 AE014185
VERSION     AE014834.1  GI:23495173
KEYWORDS    .
SOURCE      Plasmodium falciparum 3D7
  ORGANISM  Plasmodium falciparum 3D7
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 253001)
  AUTHORS   Gardner,M.J., Hall,N., Fung,E., White,O., Berriman,M., Hyman,R.W.,
            Carlton,J.M., Pain,A., Nelson,K.E., Bowman,S., Paulsen,I.T.,
            James,K., Eisen,J.A., Rutherford,K., Salzberg,S.L., Craig,A.,
            Kyes,S., Chan,M.-S., Nene,V., Shallom,S.J., Suh,B., Peterson,J.,
            Angiuoli,S., Pertea,M., Allen,J., Selengut,J., Haft,D.,
            Mather,M.W., Vaidya,A.B., Martin,D.M.A., Fairlamb,A.H.,
            Fraunholz,M.J., Roos,D.S., Ralph,S.A., McFadden,G.I.,
            Cummings,L.M., Subramanian,G.M., Mungall,C., Venter,J.C.,
            Carucci,D.J., Hoffman,S.L., Newbold,C., Davis,R.W., Fraser,C.M. and
            Barrell,B.
  TITLE     Genome sequence of the human malaria parasite Plasmodium falciparum
  JOURNAL   Nature 419 (6906), 498-511 (2002)
   PUBMED   12368864
REFERENCE   2  (bases 1 to 253001)
  AUTHORS   Gardner,M.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2002) The Institute for Genomic Research, 9712
            Medical Center Dr., Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .253001
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                     /isolate="3D7"
                     /db_xref="taxon:36329"
                     /chromosome="10"
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                     ENHTEDETDHEQNYEKYNVKLKNYVQNHNTQQMDKYQINEKNNISKLKQYNNNNDNNN
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                /rpt_unit="(TAAAAA)n"
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gene            <5162. .>8973
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mRNA            join(<5162. .5350,5488. .5535,5617. .5802,5902. .5981,
                6099. .6162,6254. .6349,6463. .6540,6727. .>8973)
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CDS             join(5162. .5350,5488. .5535,5617. .5802,5902. .5981,
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  Best Local Similarity   46.8%;  Pred. No. 0.61;
  Matches  216;  Conservative    0;  Mismatches  245;  Indels    1;  Gaps    1;

Qy        758 CTAAAACTTCTATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTAT 817
              || | |  | |||||  ||  | | | | |     || ||  ||| ||   |  ||||||
Db     227329 CTGATATATATATATAATATATATATTTACACAATTTCCTTTTTTTTTTTTTTTTCTAT 227388

Qy        818 TCTTGTTGGAAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTT 877
              | || ||  ||||   | |||   ||| ||  |   || ||     | |||    |   |
Db     227389 TTTTTTTACAAATACAGTAAAATTAATAAATATTCGAAAAAAGTGTATTTTGTTTTCCGT 227448

Qy        878 CGAACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTAT 937
                || || ||||     ||          |    |||        || || | | || |||
Db     227449 TTAAAAT-AAATTTGAACATTTTTTTTTTTCTTTATTTTTTATTTTGTTTGTATTTAA 227507

Qy        938 TATGGGTGGTATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAG 997
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Db      227508 ATGGAAAGTAAAAAAAAATTTTATATTTAATAATTTTTACCAATTTTTTATAGTATATAA 227567

Qy         998 ATTACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCA 1057

Db      227568 AATATGACATTTGTTTTTATTTATTTTTATTTAATTATATTTTATTCTTCTATTTAATAT 227627

Qy        1058 TGAAGGACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCA 1117

Db      227628 TTTTTGTTTGTTGTTTGTTTGTTTTATTTTTTACAGTTATATTTATATATTATATATACA 227687

Qy        1118 TATTTTATTAGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACT 1177

Db      227688 TAATATTTGTATATAAAAAAATATAAAGTGTAATTTTTTTTTAATTTTTTTTTGTTAAC 227747

Qy        1178 TTTTAATCTGAGAAAACAGTCTTAACAAAAAAAAAAAAAAAA 1219

Db      227748 ATTGCTTAATAAATAGTATTCTAATAAATAAATAAATAAATA 227789


RESULT 10
AF324424/c
LOCUS       AF324424               3026 bp    DNA     linear   INV 27-FEB-2002
DEFINITION  Ichthyophthirius multifiliis immobilization antigen isoform
            (IAG52A) gene, complete cds.
ACCESSION   AF324424
VERSION     AF324424.1  GI:12698726
KEYWORDS    .
SOURCE      Ichthyophthirius multifiliis
  ORGANISM  Ichthyophthirius multifiliis
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE   1  (bases 1 to 3026)
  AUTHORS   Lin,Y., Lin,T.L., Wang,C.C., Wang,X., Stieger,K., Klopfleisch,R.
            and Clark,T.G.
  TITLE     Variation in primary sequence and tandem repeat copy number among
            i-antigens of Ichthyophthirius multifiliis
  JOURNAL   Mol. Biochem. Parasitol. 120 (1), 93-106 (2002)
  MEDLINE   21839613
   PUBMED   11849709
REFERENCE   2  (bases 1 to 3026)
  AUTHORS   Lin,Y., Lin,T.-L. and Clark,T.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-NOV-2000) Microbiology and Immunology, NYSCVM Cornell
            University, Ithaca, NY 14853, USA
FEATURES             Location/Qualifiers
     source          1. .3026
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                     /mol_type="genomic DNA"
                     /serotype="D"
                     /isolate="G5"
                     /db_xref="taxon:5932"
     gene            1285. .2817
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     CDS             1330. .2736
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                     /note="52 kDa protein"
                     /codon_start=1
                     /transl_table=6
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                     NPGNSTCLPCPANKDYGAEATAGGAATLAKQCNIACPDGTAIASGATNYVILQTECLN
                     CAANFYFDGNNFQAGSSRCKACPANKVQGAVATAGGTATLIAQCALECPAGTVLTDGT
                     TSTYKQAASECVKCAANFYTTKQTDWVAGIDTCTSCNKKLTSGAEANLPESAKKNIQC
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ORIGIN

  Query Match             4.7%;  Score 57.8;  DB 3;  Length 3026;
  Best Local Similarity   44.0%;  Pred. No. 1.6;
  Matches  341;  Conservative    0;  Mismatches  427;  Indels    7;  Gaps    2;

Qy         445 TTCTTGTCTTAATGCAAATCATCAGTGGTTGGATTGGTCACTCTATGAACCACAATCGTA 504

Db        1325 TTTTTAAATATATATAAATAATAATTTATGGAATTTTATATGAAATAAATATAATTATTA 1266

Qy         505 ACCCTATATTAAGAAAATTCGCTTTAGTCTACGCTCCTCTTTGTGGTGGTTTCTCTAATA 564

Db        1265 ATAAAATTTTATTTTTAATAACTCTAAAATAAATTTATTTAGATATTAGTTATCTTAATG 1206

Qy         565 AATGGTGGGGTAGGAAGCACAATCAACATCATATGTTCACAAACAACATTCTAAAGGACG 624

Db        1205 TTTAGATTTTTAATAAATAAAATATTATTATTTATATTGTATTACATATGCTTTTTTTAA 1146

Qy         625 AAGATATCTAACACGATTACAAATTGTGGTAATTCCCCTTCTTATTTTTAAAGTGGAAAT 684

Db        1145 AAAAAAATTAATCATACAATAATTTTTATGAAATTAATAATTAATTTTTTATTTATATTT 1086

Qy         685 TAGACTCCATCTTAGCTTCTTATTATGAATTTGAAGGAATCTTCCTTGCCTTGCACTGGG 744

Db        1085 TTATAAATATTTTTTCTTCTAAAAATTTATAATAATTTTTATATTGTACTTATTACTTAT 1026

Qy         745 TATTATTATTCAACTAAAACTTCTATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCT 804

Db        1025 ATTATTTCTTTTAATAAAAATAAGATATCATAAAATTATGAATTTTAAATTTTTTTTTGT 966

Qy         805 TCAGTGCTTCTATTCTTGTTGGAAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCA 864

Db        965 ATAATGATTTTTATATTATCCTAAATAATTAATATACAATATTATTTTAATTATTTTATT 906

Qy         865 CTTTACCATTT-TTCGAACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACATA 923

Db        905 TTTTATAAATTATATTCACATTTTAAAAATTATAGTGATGTCAACATTATGACTGATTAA 846

Qy         924 TTCTCTCTACTTATTATGGGTGGTATGTAATATTAGACTGAACATCACTTTTTCCCATAA 983

Db        845 TATTACATATTCTTCTGTATTTTCAAAAATAAATAGTCAGAATAAAAAAATTAGTTATAT 786

Qy         984 ATTCCTTTCTACAGATTACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGG 1043

Db        785 AGCACAAACATCAATATAATAATTTTGTTATTTATTTCAAATTAAAAAATTATATATTGA 726

Qy        1044 AACCTTAAGATTCATGAAGGACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAAAT 1103

Db         725 AAGATTTATTCTTTTGAA------ATTTAAATAAATTATTTATATGGAATAGCAATTAAA 672

Qy        1104 TTATTTTAAATGCATATTTTATTAGTAATACTAACAATTGTAGGAAATGTGTTATGGTTT 1163

Db         671 TATGTAAAAATAATAAAATATAAATTTCTAATGTATAAAAAACAAAATATTATATAATTA 612

Qy        1164 GTTTACTTATTACTTTTTAATCTGAGAAAACAGTCTTAACAAAAAAAAAAAAAAA 1218

Db         611 ATTAAATAATAAATTACAAATAATATTTAATATTTTATTTAAATAAAATTAAAAA 557


RESULT 11
AX598900/c
LOCUS       AX598900               8056 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 240 from Patent WO02077272.
ACCESSION   AX598900
VERSION     AX598900.1  GI:28399038
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
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          Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
          Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
          Pelet,C. and Ziebarth,H.
  TITLE   Methods and nucleic acids for the analysis of hematopoietic cell
          proliferative disorders
  JOURNAL Patent: WO 02077272-A 240 03-OCT-2002;
          Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .8056
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo sapiens)"
ORIGIN

  Query Match             4.7%;  Score 57.4;  DB 6;  Length 8056;
  Best Local Similarity   44.3%;  Pred. No. 1.6;
  Matches  283;  Conservative    0;  Mismatches  351;  Indels    5;  Gaps    1;

Qy        586 ATCAACATCATATGTTCACAAACAACATTCTAAAGGACGAAGATATCTAACACGATTACA 645
              || || |   ||| |    ||  |   || | ||  |  || |     |||    | | |
Db       2746 ATTAATAATTTATTTAACGAATTATTTTTATTAAAAAAAAAAAATAATAAATTTAAAAAA 2687

Qy        646 AATTGTGGTAATTCCCCTTCTTATTTTTAAAGTGGAAATTAGACTCCATCTTAGCTTCTT 705
              | ||         |      || | |  ||| || |    ||        |    | ||   || ||
Db       2686 ATTTAAAAATTTATTATTTTTAAAATTTTAAATTTTAACGTTTTTTTTTATTTTTTTTTT 2627

Qy        706 ATTATGAATTTGAAGGAATCTTCCTTGCCTTGCACTGGGTATTATTATTCAACTAAAACT 765
              | |   ||||  |   ||  |  ||   ||     |  ||||| || ||  |
Db       2626 TTAAATTATTTATATTTATAATTTTTTTTTCGTTTATTTTTTATTTTTTAAAAATTTTA 2567

Qy        766 TCTATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTATTCTTGTTG 825
              | || ||  | |   ||| | | ||  ||  |  |||  |    |  || | |  || | |
Db       2566 TTTAAATTTTTAAATTTTTTAATTTATTTTATAATTTAATTTATTTTTTTTTATTTTTCG 2507

Qy        826 GAAA-----TCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGA 880
                ||      | || |   | ||| |||||   ||| || |   |  | | |  ||      |
Db       2506 TTAATATTTTAATTATTTTAAAACGAAATAATAAAAAATATATAAATAAAAATAAAAAAA 2447

Qy        881 ACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTAT 940
              | | | |     |   | ||| ||   |||     |  |          || | |   |
Db       2446 AATTAATTTTTAAAAATAAATAAATTATTTTTTTTTTAATTTTCGAAAAATAATAAAATT 2387

Qy        941 GGGTGGTATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATT 1000
                |   | |       | |   || || |  |||     || || |     | ||    |
Db       2386 TAATAAATTATTTATAAAAATAAAAAATTATATTTAAAAATTAAATAAAATTTATTTAAA 2327

Qy       1001 ACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGA 1060
              | |||  |  |    || ||    || || ||||  |     |     |    ||
Db       2326 TACGAAAATTAATAAATTATTTTAAAAATAAATAAATTAAAAAATTAAAATTTTTTTAAT 2267

Qy       1061 AGGACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATAT 1120
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Db       2266 TTATTTTAAATATTAAAAAATAAATTTTTATTAAAATTAAATTTTTTTTTTTTTTTATTT 2207

Qy       1121 TTTATTAGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTT 1180
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Db       2206 TTTTTTTCGTTTTTTTAAATTTTTAATAAAATTATAATTTTTTTTTTTTTTTATTTTTTAT 2147

Qy       1181 TAATCTGAGAAAACAGTCTTAACAAAAAAAAAAAAAAAA 1219
              |  |   | || | |   |||  ||||  | |  ||| |
Db       2146 TTTTAATAAAATAAAAAATTATTAAAATTATATTAAATA 2108


RESULT 12
AC116979/c
LOCUS       AC116979              331039 bp    DNA     linear   INV 21-FEB-2004
DEFINITION  Dictyostelium discoideum chromosome 2 map 6445720-6776760 strain
            AX4, complete sequence.
ACCESSION   AC116979
VERSION     AC116979.3  GI:42733765
KEYWORDS    HTG.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 331039)
  AUTHORS   Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P.,
            Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K.,
            Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
            Noegel,A.A.
  TITLE     Sequence and analysis of chromosome 2 of Dictyostelium discoideum
  JOURNAL   Nature 418 (6893), 79-85 (2002)
  MEDLINE   22092622
   PUBMED   12097910
  REMARK    The Dictyostelium Genome Sequencing Consortium
REFERENCE   2  (bases 1 to 331039)
  AUTHORS   Baumgart,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-APR-2002) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenberstr. 11, Jena 07745, Germany
REFERENCE   3  (bases 1 to 331039)
  AUTHORS   Baumgart,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-MAR-2003) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenberstr. 11, Jena 07745, Germany
REFERENCE   4  (bases 1 to 331039)
  AUTHORS   Baumgart,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenberstr. 11, Jena 07745, Germany
REFERENCE   5  (bases 1 to 331039)
  AUTHORS   Baumgart,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-FEB-2004) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenberstr. 11, Jena 07745, Germany
COMMENT     On Feb 21, 2004 this sequence version replaced gi:28829703.
            CDS predictions from GeneID do not necessarily reflect true genes.
            Further Information is available from IMB Jena, Department of
            Genome Analysis
            (http://genome.imb-jena.de/dictyostelium/)
            and the Univerity Colonge, Institute for Biochemistry I
            (http://www.uni-koeln.de/dictyostelium/project.shtml
            Funding
            Agency : Deutsche Forschungsgemeinschaft (DFG).
FEATURES             Location/Qualifiers
     source          1. .331039
                     /organism="Dictyostelium discoideum"
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                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /chromosome="2"
                     /map="6445720-6776760"
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                     /codon_start=1
                     /product="hypothetical protein"
                     /protein_id="AAS38697.1"
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                     LKGNGGKDATQEFDDVGHSASAIAKMQSLRIGRIEGAKPREEKKKEIKKTTTTSAPK
                     QQESAGLGLLKIPLIIIVLAIAAYFFMGDQQ"
     CDS             complement(join(2345. .3098,3189. .3526))
                     /note="GeneID exon scores (in order of location ranges):
                     98.40, 31.82 - GSCJ_ID dd_02784"
                     /codon_start=1
                     /product="similar to Dictyostelium discoideum (Slime
                     mold). Protein disulfide isomerase precursor"
                     /protein_id="AAO52220.2"
                     /db_xref="GI:42733767"
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                     FPTLKWFGKQSKDGEKYEQGRDLDTFINYINKQAGVNRVKGGKLAVGAGRVEQLDTIA
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Query Match 4.7%; Score 57; DB 3; Length 331039;
Best Local Similarity 43.8%; Pred. No. 0.86;
Matches 249; Conservative 0; Mismatches 320; Indels 0; Gaps 0;

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Qy      641 TTACAAATTGTGGTAATTCCCCTTCTTATTTTTAAAGTGGAAATTAGACTCCATCTTAGC 700
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Db   250435 TTCAAATTTGTATTAAATCTATCTATTTTTTTATTTTTTTTATTTTTTATTTTTTTTATT 250376

Qy      701 TTCTTATTATGAATTTGAAGGAATCTTCCTTGCCTTGCACTGGGTATTATTATTCAACTA 760
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Db   250375 TTTTTATTTATTTTTGAAATAATTGTTAATTACGATTAAGTTGTTATTTCAATTTCATTT 250316

Qy      761 AAACTTCTATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTTCAGTGCTTCTATTCT 820
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Db   250315 CTATAAATATATTTAATTTTTATTTTTTTAAATTTTTTTATTTTTTATTTTTTTATTTAT 250256

Qy      821 TGTTGGAAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCACTTTACCATTTTTCGA 880
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Db   250255 TTTTTAAAAAAAAAAAGCTTAATTATAACAAAATTTTTTATTTTTTATTTTATTTTTTTT 250196

Qy      881 ACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATTCTCTCTACTTATTAT 940
              | ||| |    ||   || || |    |||  |     | || | | |  || || |
Db   250195 TTTTAAAAAAATATCATTAAGTAATTTTTTTTTTTAATTTTTTTTTTTTTTTTTTTTTT 250136

Qy      941 GGGTGGTATGTAATATTAGACTGAACATCACTTTTTCCCATAAATTCCTTTCTACAGATT 1000
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Db     250135 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCATTAACGACCACCTT 250076

Qy       1001 ACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAACCTTAAGATTCATGA 1060

Db     250075 TTACTAATCCCAACAATTCTTATAGATATTTAATAGGTTAAAAAAAACAAACAAATTTGT 250016

Qy       1061 AGGACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTTATTTTAAATGCATAT 1120

Db     250015 ATTATTAAATAAAATAAAAAAAAAAAAAACCATTTTAAAAAAAAAAAAAGATAGAATTTTAT 249956

Qy       1121 TTTATTAGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGTTTACTTATTACTTTT 1180

Db     249955 TTTATTTTTTTTTTTTAAAAAATCAAGAAAATGTCAGATGATAAAATTCATTTAAAAGTTA 249896

Qy       1181 TAATCTGAGAAAACAGTCTTAACAAAAAA 1209

Db     249895 GATTGGTTGATAAGAAAGTTTTTAAAAAA 249867


RESULT 13
AF362375/c
LOCUS       AF362375               7079 bp    DNA     linear   INV 19-APR-2002
DEFINITION  Dictyostelium discoideum histidine kinase DhkE (dhkE) gene,
            complete cds.
ACCESSION   AF362375
VERSION     AF362375.2  GI:20198941
KEYWORDS    .
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 7079)
  AUTHORS   Anjard,C. and Loomis,W.F.
  TITLE     The histidine kinases of Dictyostelium
  JOURNAL   (in) Inouye,M. and Dutta,R. (Eds.);
            HISTIDINE KINASES IN SIGNAL TRASNDUCTION;
            Academic press, San Diego (2001) In press
REFERENCE   2  (bases 1 to 7079)
  AUTHORS   Anjard,C. and Loomis,W.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2001) Biology 0368, UCSD, 9500 Gilman Drive, La
            Jolla, CA 92093, USA
COMMENT     On Apr 19, 2002 this sequence version replaced gi:14133661.
FEATURES             Location/Qualifiers
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     misc_feature    2873. .3736
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                     /note="Region: catalytic domain"
     misc_feature    5615. .5971
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                     /note="Region: receiver domain"
ORIGIN

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  Best Local Similarity   47.0%;  Pred. No. 2;
  Matches  207;  Conservative    0;  Mismatches  232;  Indels    1;  Gaps    1;

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Db        791 ATTATTATTAATTTTTAATTTATCCATATTAATTCTATTTTTTTAAATTTATAGGTTATT 732

Qy        806 CAGTGCTTCTATTCTTGTTGGAAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCAC 865

Db        731 TTATAAATTTACTTTCTCTTTAAATAATAAATAGAAAAAAAATTGAGGAAAAAAAAAAAA 672

Qy        866 TTTACCATTTTTCGAACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATT 925

Db        671 AAAAAAAAAAAGGACCCACCCATCAAAAGAAAGTGATTGGTATTTTTTTTATTTTTTTTT 612

Qy        926 CTCTCTA-CTTATTATGGGTGGTATGTAATATTAGACTGAACATCACTTTTTCCCATAAA 984

Db        611 CTTCAAATATTATTTAATTTCCCTTTTTTTTTTTTTTTAATTGAAAAATATTTATCATAAA 552

Qy        985 TTCCTTTCTACAGATTACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGA 1044

Db        551 TAATTTAAAATAAAACCAAATCAGATCAAATCAAAAAAAAAAAAAAAAATAAAATTGTGTA 492

Qy       1045 ACCTTAAGATTCATGAAGGACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATT 1104

Db        491 TGCCAAATATTTTTAAAAAATTGTTATTTTTACTTTCACTAATGTATTAATGTTTATTAT 432

Qy       1105 TATTTTAAATGCATATTTTATTAGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTG 1164

Db        431 TATTATAATTATTATTTTTATTATTATTTTTATTATTTATTTATTTTTATTATTATTATT 372

Qy       1165 TTTACTTATTACTTTTTAAT 1184

Db        371 ATTATTATTATTATTTTTAT 352


RESULT 14
CR387984
LOCUS       CR387984              159835 bp    DNA     linear   HTG 19-APR-2004
DEFINITION  Danio rerio clone DKEY-230E6, *** SEQUENCING IN PROGRESS ***, 6
            unordered pieces.
ACCESSION   CR387984
VERSION     CR387984.3  GI:46408734
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
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          Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
          Cypriniformes; Cyprinidae; Danio.
REFERENCE 1  (bases 1 to 159835)
  AUTHORS   McLay,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-2004) Wellcome Trust Sanger Institute, Hinxton,
          Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
          zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT   On Apr 19, 2004 this sequence version replaced gi:46358283.
          -------------- Genome Center
          Center: Wellcome Trust Sanger Institute
          Center code: SC
          Web site: http://www.sanger.ac.uk
          Contact: zfish-help@sanger.ac.uk
          -------------- Project Information
          Center project name: zK230E6
          -------------- Summary Statistics
          Assembly program: XGAP4; version 4.5
          Chemistry: Dye-terminator; 100% of reads
          Consensus quality: 157552 bases at least Q40
          Consensus quality: 157753 bases at least Q30
          Consensus quality: 157954 bases at least Q20
          Insert size: 159335; sum-of-contigs
          Insert size: 161212; 5.4% error; agarose-fp
          Quality coverage: 8.49x in Q20 bases; sum-of-contigs Quality
          coverage: 8.53x in Q20 bases; agarose-fp
          --------------.
          * NOTE: This is a 'working draft' sequence. It currently
          * consists of 6 contigs. The true order of the pieces
          * is not known and their order in this sequence record is
          * arbitrary. Gaps between the contigs are represented as
          * runs of N, but the exact sizes of the gaps are unknown.
          * This record will be updated with the finished sequence
          * as soon as it is available and the accession number will
          * be preserved.
          *       1    83704: contig of 83704 bp in length
          *   83705    83804: gap of 100 bp
          *   83805    90391: contig of 6587 bp in length
          *   90392    90491: gap of 100 bp
          *   90492    95482: contig of 4991 bp in length
          *   95483    95582: gap of 100 bp
          *   95583   120943: contig of 25361 bp in length
          *  120944   121043: gap of 100 bp
          *  121044   151145: contig of 30102 bp in length
          *  151146   151245: gap of 100 bp
          *  151246   159835: contig of 8590 bp in length.
FEATURES             Location/Qualifiers
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     misc_feature    1. .83704
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     misc_feature    83805. .90391
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     misc_feature    90492. .95482
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     misc_feature    95583. .120943
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     misc_feature    121044. .151145
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ORIGIN

  Query Match             4.7%;  Score 56.8;  DB 2;  Length 159835;
  Best Local Similarity   42.6%;  Pred. No. 1.1;
  Matches  202;  Conservative    0;  Mismatches  272;  Indels    0;  Gaps    0;

Qy        746 ATTATTATTCAACTAAAACTTCTATATCGTAATTCTTTCTGAATTGATTGCTGGTTTCTT 805
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Db        376 ATTAATAAAAAAATAAAAANNNNAAAANATATTTTTATTTTTTATTTTATTTAATAATT 435

Qy        806 CAGTGCTTCTATTCTTGTTGGAAATCATGAAAATGAAATGAAATTCGAAAGAAGAATCAC 865
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Db        436 TATTTTTTTTTTTAAAAAATTAATTTATTNTATANATATATATATATANATATATATA 495

Qy        866 TTTACCATTTTTCGAACATCAAATAGCTGCAAGCAGAAACTACGCTTTCCACGACATATT 925
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Db        496 AAAATAAATAAATAAATATNNATATATANANANTAAAAAAAAAATTTNNNAANNTANTTA 555

Qy        926 CTCTCTACTTATTATGGGTGGTATGTAATATTAGACTGAACATCACTTTTTCCCATAAAT 985
              | | |   | |  |   | | |  |||| | | ||    |  |       |||  |
Db        556 TTTTTTTTNTNTNTTTNTTTTTTTATTTAATTATATTAAAATATATATANAAATATATTT 615

Qy        986 TCCTTTCTACAGATTACCCAAAGCTCGTGTCATAATTGCTGAAGAATTAAAGAAGTGGAA 1045
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Db        616 ATTTNTATTAAAAAAATAAAANANTTTTATAAATAAAANTNAAAAATAAATAAATAAAAA 675

Qy       1046 CCTTAAGATTCATGAAGGACCTATTTTTGAAAAATCTCACCTTTGAAAATAAATAAATTT 1105
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Db        676 AATATATATAAATATATATATATATATATATATTTATTTTTTTTATTTTTTTATTTTT 735

Qy       1106 ATTTTAAATGCATATTTTATTAGTAATACTAACAATTGTAGGAAATGTGTTATGGTTTGT 1165
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RESULT 15
MBREV/c
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DEFINITION  Monosiga brevicollis mitochondrion, complete genome.
ACCESSION   AF538053 AF275274
VERSION     AF538053.1  GI:23344058
KEYWORDS    .
SOURCE      mitochondrion Monosiga brevicollis
  ORGANISM  Monosiga brevicollis
          Eukaryota; Choanoflagellida; Codonosigidae; Monosiga.
REFERENCE 1  (bases 64800 to 65249)
  AUTHORS   Bullerwell,C.E., Burger,G. and Lang,B.F.
  TITLE     A novel motif for identifying rps3 homologs in fungal mitochondrial
          genomes
  JOURNAL   Trends Biochem. Sci. 25 (8), 363-365 (2000)
  MEDLINE   20377911
   PUBMED   10916154
REFERENCE 2  (bases 1 to 76568)
  AUTHORS   Lang,B.F., O'Kelly,C., Nerad,T., Gray,M.W. and Burger,G.
  TITLE     The closest unicellular relatives of animals
  JOURNAL   Curr. Biol. 12 (20), 1773-1778 (2002)
  MEDLINE   22288938
   PUBMED   12401173
REFERENCE 3  (bases 64800 to 65249)
  AUTHORS   Lang,F.B. and Bullerwell,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUN-2000) Biochimie, Universite de Montreal, 2900
          Boul. Edouard Montpetit, Montreal, QUE H3C 3J7, Canada
REFERENCE 4  (bases 1 to 76568)
  AUTHORS   Burger,G. and Lang,B.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2002) Biochimie, Universite de Montreal, 2900,
          Boul. Edouard-Montpetit, Montreal, Quebec H3T 1J4, Canada
COMMENT     On Sep 29, 2002 this sequence version replaced gi:9966505.
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  Query Match             4.6%;  Score 56.4;  DB 3;  Length 76568;
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